

CAB89082.1 AJ277534 *Asparagus officinalis*  
S6 ribosomal protein kinase. pk1. putative.

AAB93862.1 U89681 *Lycopersicon esculentum*  
protein kinase. LePK4. contains catalytic domain.

BAA92972.1 AP001551 *Oryza sativa*  
ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene.  
Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F6I18 ; putative protein kinase.  
(AL022198).

BAB12687.1 AP002746 *Oryza sativa*  
putative protein kinase. P0671B11.2. contains ESTs C22394(C30013),C22393(C30013).

SEQ ID NO: 508

BAA23676.1 AB000970 *Brassica rapa*  
receptor kinase 1. BcRK1.

CAA74662.1 Y14286 *Brassica oleracea*  
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular  
kinase domain: from 1413.

CAA74661.1 Y14285 *Brassica oleracea*  
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular  
kinase domain: 1412-2554.

CAA73133.1 Y12530 *Brassica oleracea*  
serine /threonine kinase. ARLK.

CAA67145.1 X98520 *Brassica oleracea*  
receptor-like kinase. SFR2.

AAA33008.1 M97667 *Brassica napus*  
serine/threonine kinase receptor.

CAB89179.1 AJ245479 *Brassica napus* subsp. *napus*  
ser /thr kinase. S-locus receptor kinase. srk.

CAA79355.1 Z18921 *Brassica oleracea*  
S-receptor kinase-like protein.

CAB41878.1 Y18259 *Brassica oleracea*  
SRK5 protein. SRK5. receptor-like kinase.

AAA33000.1 M76647 *Brassica oleracea*  
receptor protein kinase. SKR6.

BAA92837.1 AB032474 *Brassica oleracea*  
S60 S-locus receptor kinase. SRK60.

BAA21132.1 D88193 *Brassica rapa*  
S-receptor kinase. SRK9 (B.c).

BAA06285.1 D30049 *Brassica rapa*  
S-receptor kinase SRK9.

AAA62232.1 U00443 *Brassica napus*  
S-receptor kinase. protein contains an immunoglobulin-like domain.

BAA92836.1 AB032473 *Brassica oleracea*  
S18 S-locus receptor kinase. SRK18.

BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrkl.
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAK02023.1	AC074283	Oryza sativa	Putative protein kinase-like. OSJNBa0087H07.5.
CAA79324.1	Z18884	Brassica oleracea	S-receptor kinase related protein.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
CAB51836.1	AJ243961	Oryza sativa	Putitive Ser/Thr protein kinase. I1332.7.
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
BAA92953.1	AP001551	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).

BAA92954.1	AP001551	Oryza sativa
Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).		
AAG16628.1	AY007545	Brassica napus
protein serine/threonine kinase BNK1.		
BAB16871.1	AP002537	Oryza sativa
putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).		
SEQ ID NO: 510		
AAG30254.1	AF307333	Hordeum vulgare
putative nematode-resistance protein. Hs1. similar to Beta procumbens Hs1pro protein.		
AAB48305.1	U79733	Beta procumbens
nematode resistance. Hs1pro-1.		
SEQ ID NO: 513		
BAA14144.1	D90116	Armoracia rusticana
peroxidase isozyme.		
BAA14143.1	D90115	Armoracia rusticana
peroxidase isozyme.		
BAA11853.1	D83225	Populus nigra
peroxidase.		
CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa
signal for ER. peroxidase.		
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa
signal for ER. peroxidase.		
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa
signal for ER. peroxidase.		
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa
signal for ER. peroxidase.		
BAA11852.1	D83224	Populus nigra
peroxidase.		
BAA07241.1	D38051	Populus kitakamiensis
peroxidase. prxA4a.		
BAA06335.1	D30653	Populus kitakamiensis
peroxidase.		
AAB47602.1	L07554	Linum usitatissimum
peroxidase. FLXPER1.		
AAC98519.1	AF007211	Glycine max
peroxidase precursor. GMIPER1. pathogen-induced.		
AAD37427.1	AF149277	Phaseolus vulgaris
peroxidase 1 precursor. FBP1. secretory peroxidase.		
BAA06334.1	D30652	Populus kitakamiensis
peroxidase.		
AAB97734.1	AF014502	Glycine max
seed coat peroxidase precursor. Ep. H2O2 oxidoreductase; class III plant peroxidase.		

CAB94692.1	AJ242742	<i>Ipomoea batatas</i>	Removal of H <sub>2</sub> O <sub>2</sub> , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
CAA62227.1	X90694	<i>Medicago sativa</i>	peroxidase1C. prx1C.
CAA62226.1	X90693	<i>Medicago sativa</i>	peroxidase1B. prx1B.
AAD37430.1	AF149280	<i>Phaseolus vulgaris</i>	peroxidase 5 precursor. FBP5. secretory peroxidase.
CAA62225.1	X90692	<i>Medicago sativa</i>	peroxidase1A. prx1A.
AAB41811.1	L36157	<i>Medicago sativa</i>	peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.
AAB41810.1	L36156	<i>Medicago sativa</i>	peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
BAA01877.1	D11102	<i>Populus kitakamiensis</i>	peroxidase. prxA1.
CAB67121.1	Y19023	<i>Lycopersicon esculentum</i>	peroxidase. cevi-1.
CAA50597.1	X71593	<i>Lycopersicon esculentum</i>	peroxidase. CEVI-1.
BAA01992.1	D11396	<i>Nicotiana tabacum</i>	'peroxidase'.
AAA34108.1	J02979	<i>Nicotiana tabacum</i>	lignin-forming peroxidase precursor (EC 1.11.1.7).
AAA33127.1	M91373	<i>Cucumis sativus</i>	peroxidase. pre-peroxidase. putative.
BAA92500.1	AP001383	<i>Oryza sativa</i>	ESTs D39300(R3292),AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).
CAB65334.1	AJ250121	<i>Picea abies</i>	peroxidase. SPI2 protein. spi2.
CAA40796.1	X57564	<i>Armoracia rusticana</i>	peroxidase. peroxidase precursor.
AAB06183.1	M37636	<i>Arachis hypogaea</i>	cationic peroxidase. PNC1.
CAA76680.1	Y17192	<i>Cucurbita pepo</i>	peroxidase. aprx. type III peroxidase.
AAA33129.1	M91372	<i>Cucumis sativus</i>	peroxidase. pre-peroxidase.



CAA71492.1	Y10466	Spinacia oleracea	peroxidase. prxr5.
AAF63027.1	AF244924	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
AAD43561.1	AF155124	Gossypium hirsutum	bacterial-induced peroxidase precursor. Perx_Goshiko.
AAF63026.1	AF244923	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx14 precursor. type III peroxidase.
AAA33121.1	M32742	Cucumis sativus	peroxidase (CuPer2).
BAA92422.1	AP001366	Oryza sativa	ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to A.thaliana mRNA for peroxidase ATP18a. (X98804).
BAA92497.1	AP001383	Oryza sativa	ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to peroxidase ATP18a. (X98804).
BAA77389.1	AB024439	Scutellaria baicalensis	peroxidase 3.
BAA08499.1	D49551	Oryza sativa	peroxidase. poxN.
AAB19129.1	U41657	Glycine max	seed coat peroxidase isozyme. SPOD4.1. H2O2 oxidoreductase.
BAA03373.1	D14482	Oryza sativa	putative peroxidase.
AAB02554.1	L37790	Stylosanthes humilis	cationic peroxidase.
SEQ ID NO: 515			
AAB88134.1	AF034618	Spinacia oleracea	cytosolic heat shock 70 protein. HSC70-1.
AAF34134.1	AF161180	Malus x domestica	high molecular weight heat shock protein. Hsp2.
AAB99745.1	AF005993	Triticum aestivum	HSP70. TaHSP70d. 70 kDa heat shock protein, molecular chaperone.
AAA62325.1	L32165	Hordeum vulgare	Molecular chaperone. HSP70. Heat-shock protein HSP70; The predicted amino acid sequence is highly homologous (more than 80% identity) to other plant heat-shock proteins (HSP70s) in the database; however the C terminus is quite unique.; putative.
AAA21808.1	L23551	Spinacia oleracea	molecular chaperone. ER-lumenal protein. HSC70.
AAA34139.1	L08830	Lycopersicon esculentum	molecular chaperon (precursor). glucose-regulated protein 78. BiP/grp78. an endoplasmic reticulum residing heat shock protein 70 family member; precursor peptide.

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AAB86942.1 AF031241 Glycine max  
endoplasmic reticulum transport protein; molecular chaperone; roles in protein folding, assembly, and transport. endoplasmic reticulum HSC70-cognate binding protein precursor. BiP. BiP; similar to HSC70 and GRP78.

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AAK21920.1 AF338252 Glycine max  
molecular chaperone. BiP-isoform D. BiPD. ER-lumenal HSP70; binding protein GRP78.

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AAB91473.1 AF035458 Spinacia oleracea  
heat shock 70 protein. HSC70-11. mitochondrial protein.

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AAB96660.1 AF039084 Spinacia oleracea  
heat shock 70 protein. HSC70-11. molecular chaperone.

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AAB91472.1 AF035457 Spinacia oleracea  
heat shock 70 protein. HSC70-10. mitochondrial protein.

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SEQ ID NO: 516

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CAA06927.1 AJ006233 Nicotiana tabacum  
putative thaumatin-like protein precursor.

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AAF06346.1 AF195653 Vitis vinifera  
SCUTL1. thaumatin-like protein.

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BAA28872.1 AB006009 Pyrus pyrifolia  
thaumatin-like protein precursor. PsTL1.

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CAC10270.1 AJ243427 Malus x domestica  
thaumatin-like protein. tl. allergen, pathogenesis-related.

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AAC36740.1 AF090143 Malus x domestica  
thaumatin-like protein precursor Mdtl1. MDTL1. pathogenesis-related.

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CAB62167.1 AJ242828 Castanea sativa  
antifungal. thaumatin-like protein. tl1.

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AAB38064.1 U32440 Prunus avium  
thaumatin-like protein precursor.

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BAA74546.2 AB000834 Nicotiana tabacum  
thaumatin-like protein SE39b.

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AAF06347.1 AF195654 Vitis vinifera  
SCUTL2. thaumatin-like protein.

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CAC09477.1 AL442113 Oryza sativa  
thaumatin-like protein. H0806H05.10.

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AAB95118.1 U71244 Brassica rapa  
pathogenesis-related group 5 protein. BFTP. thaumatin-like protein; PR-5.

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CAA10492.1 AJ131731 Pseudotsuga menziesii  
Thaumatin-like protein. 5A1A.16.

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BAA95017.1 AB031870 Cestrum elegans  
thaumatin-like protein. CETLP.

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BAA95165.1 AB029918 Nicotiana tabacum  
pistil transmitting tissue specific thaumatin (SE39b)-like protein. SE39b.

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AAB61590.1 AF003007 Vitis vinifera  
VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.

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AAD55090.1	AF178653	Vitis riparia	thaumatin. osmotin; pathogenesis-related protein.
CAB85637.1	AJ237999	Vitis vinifera	putative thaumatin-like protein. T11. alternative name grip 51.
AAF82264.1	AF227324	Vitis vinifera	thaumatin-like protein.
AAB02259.1	U57787	Avena sativa	permatin precursor. thaumatin-like protein.
AAB53368.1	U77657	Oryza sativa	pathogenesis-related thaumatin-like protein.
CAA09228.1	AJ010501	Cicer arietinum	thaumatin-like protein PR-5b.
CAA33293.1	X15224	Nicotiana tabacum	thaumatin-like protein. E22.
CAA33292.1	X15223	Nicotiana tabacum	thaumatin-like protein. E2.
SEQ ID NO: 517			
CAA71801.1	Y10848	Brassica juncea	gamma-glutamylcysteine synthetase. gsh1.
AAB71230.1	AF017983	Lycopersicon esculentum	gamma-glutamylcysteine synthetase. GSH1.
AAC82334.1	AF041340	Medicago truncatula	gamma-glutamylcysteine synthetase. putative plastid protein.
AAF22137.1	AF128455	Pisum sativum	gamma-glutamylcysteine synthetase precursor. gsh1. putative plastid protein.
AAF22136.1	AF128454	Phaseolus vulgaris	gamma-glutamylcysteine synthetase precursor. gsh1. putative plastid protein.
CAA06613.1	AJ005587	Brassica juncea	gamma-glutamylcysteine synthetase.
AAG13459.1	AF128453	Glycine max	gamma-glutamylcysteine synthetase precursor. gsh1.
CAA64808.1	X95563	Brassica juncea	gamma-glutamylcysteine synthetase. gsh1.
SEQ ID NO: 518			
AAA75414.1	L28005	Glycine max	TGACG-motif-binding protein. STGA1.
AAB31250.2	S73827	Solanum tuberosum	mas-binding factor MBF3. transcription factor TGA1a homolog; This sequence comes from Fig. 4.
AAB31249.1	S73826	Solanum tuberosum	mas-binding factor MBF2. mas-binding factor MBF2. transcription factor TGA1a homolog; This sequence comes from Fig. 4.

CAA34468.1	X16449	Nicotiana sp.	TGA1a protein (AA 1-359).
AAA34091.1	M62855	Nicotiana tabacum	ASF-1/G13. leucine-zipper DNA-binding protein.
AAB31251.2	S73828	Solanum tuberosum	mas-binding factor MBF1. transcription factor TGA1a homolog; This sequence comes from Fig. 4.
CAA48904.1	X69152	Zea mays	ocs-element binding factor 3.2. OBF3.2.
CAA48905.1	X69153	Zea mays	ocs-element binding factor 3.1. OBF3.1.
AAC24123.1	AF067187	Cichorium intybus	cAMP responsive element binding protein. bZIP transcription factor; CREB.
AAC24122.1	AF067186	Cichorium intybus	cAMP responsive element binding protein. CREB1.
AAC49760.1	AF001454	Helianthus annuus	Dc3 promoter-binding factor-2. DPBF-2.
SEQ ID NO: 521			
CAA10608.1	AJ132228	Ricinus communis	amino acid carrier. aap3.
CAA07563.1	AJ007574	Ricinus communis	amino acid carrier. aap1.
CAA70778.1	Y09591	Vicia faba	amino acid transporter.
AAD16014.1	AF080543	Nepenthes alata	amino acid transporter. AAP2.
CAA70969.1	Y09826	Solanum tuberosum	amino acid transporter. AAP2. transmembrane protein.
AAD16015.1	AF080544	Nepenthes alata	amino acid transporter. AAP3.
CAA70968.1	Y09825	Solanum tuberosum	amino acid transporter. AAP1. transmembrane protein.
CAA92992.1	Z68759	Ricinus communis	amino acid carrier.
AAD16013.1	AF080542	Nepenthes alata	amino acid transporter. AAP1.
AAF15945.1	AF061435	Vicia faba	amino acid transporter b. AAPB.
CAA72006.1	Y11121	Ricinus communis	amino acid carrier.
AAF15944.1	AF061434	Vicia faba	amino acid transporter a. AAPA.

AAF15946.1	AF061436	Vicia faba	amino acid transporter c. AAPC.
AAB48944.1	U31932	Nicotiana sylvestris	amino acid permease 1. NSAAP1. amino acid transporter; Method: conceptual translation supplied by author.
AAB96830.1	U64823	Nicotiana sylvestris	amino acid transporter. amino acid permease. nsaap1.
BAA93437.1	AB022783	Oryza sativa	amino acid permease. OsproT.
AAD25162.1	AF014810	Lycopersicon esculentum	proline transporter 3. LeProT3.
AAD25161.1	AF014809	Lycopersicon esculentum	proline transporter 2. LeProT2.
AAD25160.1	AF014808	Lycopersicon esculentum	proline transporter 1. LeProT1.
AAF76897.1	AF274032	Atriplex hortensis	proline/glycine betaine transporter.
CAB42599.1	AJ238635	Chlorella protothecoides	amino acid carrier. dee4.
SEQ ID NO: 526			
BAA03763.1	D16247	Nicotiana sylvestris	RNA helicase like protein DB10.
AAD46404.1	AF096248	Lycopersicon esculentum	ethylene-responsive RNA helicase. ER68. putative DEAD box/RNA helicase.
AAF75791.1	AF271892	Pisum sativum	DEAD box protein P68. P68. RNA helicase.
AAF40306.1	AF156667	Vigna radiata	RNA helicase. VRH1.
CAA68193.1	X99937	Spinacia oleracea	RNA helicase. prh75. DEAD-box protein; homologous to X99938.
AAG13612.1	AC078840	Oryza sativa	putative RNA helicase. OSJNBb0073N24.12.
AAG34876.1	AF261021	Nicotiana tabacum	putative chloroplast RNA helicase VDL isoform 1. VDL. alternatively spliced.
AAG34873.1	AF261020	Nicotiana tabacum	putative chloroplast RNA helicase VDL isoform 1. VDL. essential for chloroplast development; may be involved in post-transcriptional regulation.
AAG34879.1	AF261024	Nicotiana tabacum	putative chloroplast RNA helicase VDL' isoform 1. VDL'. alternatively spliced.
AAD20980.1	AF079782	Zea mays	ATPase and RNA helicase. translation initiation factor 4A2. tif4A2.
AAG34882.1	AF261027	Nicotiana tabacum	putative chloroplast RNA helicase VDL' isoform 4. VDL'. alternatively spliced.

BAA95705.1	AB042644	Oryza sativa
DEAD box RNA helicase OsPL10b. OsPL10b.		
BAA95704.1	AB042643	Oryza sativa
DEAD box RNA helicase OsPL10a. OsPL10a.		
AAG34883.1	AF261028	Nicotiana tabacum
putative chloroplast RNA helicase VDL' isoform 5. VDL'. alternatively spliced.		
AAG34893.1	AF261032	Nicotiana tabacum
putative chloroplast RNA helicase VDL' isoform 1. VDL'. alternatively spliced.		
AAG34884.1	AF261029	Nicotiana tabacum
putative chloroplast RNA helicase VDL' isoform 6. VDL'. alternatively spliced.		
AAG34896.1	AF261032	Nicotiana tabacum
putative chloroplast RNA helicase VDL' isoform 4. VDL'. alternatively spliced.		
AAG34897.1	AF261032	Nicotiana tabacum
putative chloroplast RNA helicase VDL' isoform 5. VDL'. alternatively spliced.		
AAG34898.1	AF261032	Nicotiana tabacum
putative chloroplast RNA helicase VDL' isoform 6. VDL'. alternatively spliced.		
AAG38500.1	AF261032	Nicotiana tabacum
putative chloroplast RNA helicase VDL' isoform 8. VDL'. alternatively spliced.		
AAG34886.1	AF261031	Nicotiana tabacum
putative chloroplast RNA helicase VDL' isoform 8. VDL'. alternatively spliced.		
AAG48833.1	AC084218	Oryza sativa
similar to Arabidopsis thaliana DNA helicase (AJ404475).		
SEQ ID NO: 528		
CAA65536.1	X96761	Sporobolus stapfianus
sulphate transporter protein.		
AAK27688.1	AF347614	Lycopersicon esculentum
sulfate transporter 2. ST2.		
AAK27687.1	AF347613	Lycopersicon esculentum
sulfate transporter 1. ST1.		
CAA57711.1	X82256	Stylosanthes hamata
high affinity sulphate transporter. SHST2.		
AAG41419.1	AF309643	Solanum tuberosum
high affinity sulfate transporter type 1. ST1.		
CAA57710.1	X82255	Stylosanthes hamata
high affinity sulphate transporter. SHST1.		
AAK35215.1	AF355602	Zea mays
sulfate transporter ST1.		
CAA65291.1	X96431	Hordeum vulgare
high affinity sulphate transporter. HVST1.		
AAA97952.1	U52867	Hordeum vulgare
high affinity sulfate transporter HVST1.		

CAB42985.1	AJ238244	<i>Aegilops tauschii</i> putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st1.
CAB42986.1	AJ238245	<i>Aegilops tauschii</i> putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st2.
CAA57831.1	X82454	<i>Stylosanthes hamata</i> low affinity sulphate transporter. SHST3.
SEQ ID NO: 531		
AAK00436.1	AC060755	<i>Oryza sativa</i> putative zinc finger protein. OSJNBa0003O19.23.
BAA85438.1	AP000616	<i>Oryza sativa</i> similar to RING-H2 finger protein RHA1a (AF078683).
AAG43550.1	AF211532	<i>Nicotiana tabacum</i> Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.
BAA90357.1	AP001080	<i>Oryza sativa</i> EST AU070319(S10788) corresponds to a region of the predicted gene. Similar to RING-H2 finger protein RHA2b (AC006200).
SEQ ID NO: 532		
BAA81751.1	AB017517	<i>Marchantia polymorpha</i> calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
BAA13232.1	D87042	<i>Zea mays</i> Calcium-dependent protein kinase.
BAA81749.1	AB017515	<i>Marchantia polymorpha</i> calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
BAA81750.1	AB017516	<i>Marchantia polymorpha</i> calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
BAA85396.1	AP000615	<i>Oryza sativa</i> ESTs C22369(C12239),C22370(C12239), AU057852(S21844),AU057853(S21844) correspond to a region of the predicted gene.; similar to calcium dependent protein kinase. (AF048691).
CAA57156.1	X81393	<i>Oryza sativa</i> calcium-dependent protein kinase. OSCPCKII.
AAC05270.1	AF048691	<i>Oryza sativa</i> calcium dependent protein kinase. CDPK12.
AAB49984.1	U90262	<i>Cucurbita pepo</i> calcium-dependent calmodulin-independent protein kinase CDPK. cpCPK1. serine/threonine protein kinase that is activated by direct binding of calcium.
AAB70706.1	U82087	<i>Tortula ruralis</i> calmodulin-like domain protein kinase. TrCPK1.
AAG46110.1	AC073166	<i>Oryza sativa</i> calcium-dependent protein kinase. OSJNBb0064P21.2.
BAA02698.1	D13436	<i>Oryza sativa</i> calcium-dependent protein kinase. spk.

BAA81748.1	AB017515	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
CAA07481.1	AJ007366	Zea mays	calcium-dependent protein kinase.
AAB80692.1	U69173	Glycine max	calmodulin-like domain protein kinase isoenzyme beta. CDPK beta.
AAC49405.1	U08140	Vigna radiata	calcium dependent protein kinase. CDPK.
BAA12338.1	D84408	Zea mays	calcium dependent protein kinase. ZmCDPK1.
AAA33443.1	L15390	Zea mays	calcium-dependent protein kinase. CDPK.
CAA57157.1	X81394	Oryza sativa	calcium-dependent protein kinase. OSCPK2.
BAB21081.1	AP002819	Oryza sativa	putative calcium-dependent protein kinase. P0501G01.10.
BAA12715.1	D85039	Zea mays	calcium-dependent protein kinase.
CAA65500.1	X96723	Medicago sativa	protein kinase. CDPK.
AAC25423.1	AF072908	Nicotiana tabacum	calcium-dependent protein kinase. CDPK1.
AAA69507.1	U28376	Zea mays	calcium-dependent protein kinase. MZECDPK2.
BAA13440.1	D87707	Ipomoea batatas	calcium dependent protein kinase. CDPK.
AAD28192.2	AF115406	Solanum tuberosum	calcium-dependent protein kinase. CDPK; catalytic domain.
AAB80693.1	U69174	Glycine max	calmodulin-like domain protein kinase isoenzyme gamma. CDPK gamma.
AAA61682.1	L27484	Zea mays	calcium-dependent protein kinase. CDPK.
AAD17800.1	AF090835	Mesembryanthemum crystallinum	Ca <sup>2+</sup> -dependent protein kinase. CPK1. serine/threonine protein kinase.
CAA39936.1	X56599	Daucus carota	calcium- dependent protein kinase. DcPK431.
AAK26164.1	AY027885	Cucumis sativus	calcium-dependent calmodulin-independent protein kinase 5. CDPK5. CsCDPK5.
AAB88537.1	AF035944	Fragaria x ananassa	calcium-dependent protein kinase. MAX17.
AAF21062.1	AF216527	Dunaliella tertiolecta	calcium-dependent protein kinase. CPK1; CDPK.



CAA89202.1	Z49233	Chlamydomonas eugametos	calcium-stimulated protein kinase.
AAC32116.1	AF051211	Picea mariana	probable calcium dependent protein kinase. Sb15. similar to Vigna radiata calcium dependent protein kinase encoded by U08140.
AAF23900.1	AF194413	Oryza sativa	calcium-dependent protein kinase. CDPK1. OsCDPK1.
AAF23901.2	AF194414	Oryza sativa	calcium-dependent protein kinase. CDPK5. OsCDPK5.
CAB46228.1	Y18055	Arachis hypogaea	calcium dependent protein kinase. CDPK.
AAC78558.1	AF030879	Solanum tuberosum	protein kinase CPK1.
CAA58750.1	X83869	Daucus carota	CDPK-related protein kinase. CRK (or PK421).
AAB47181.1	S82324	Zea mays	/gene="calcium/calmodulin-dependent protein kinase. This sequence comes from Fig. 1.
BAA12691.1	D84507	Zea mays	CDPK-related protein kinase. Does not require calcium for its activity (by similarity).
BAA22410.1	D38452	Zea mays	calcium-dependent protein kinase-related kinase.
BAA12692.1	D84508	Zea mays	CDPK-related protein kinase. Does not require calcium for its activity.
AAG01179.1	AF289237	Zea mays	calcium/calmodulin dependent protein kinase MCK2. MCK2.
AAC24961.1	AF009337	Tradescantia virginiana	CDPK-related protein kinase. CRK1.
BAA90814.1	AP001168	Oryza sativa	ESTs AU030197(E50746),AU030196(E50746) correspond to a region of the predicted gene.; Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).
AAC49008.1	U24188	Lilium longiflorum	calcium/calmodulin-dependent phosphorylation activity. calcium/calmodulin-dependent protein kinase. CCaMK. serine/threonine kinase; binds to calcium and calmodulin.
AAF19402.1	AF203480	Lycopersicon esculentum	phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca <sup>2+</sup> /CaM kinase family; lacks the autoinhibitory region and EF hands.
SEQ ID NO: 535			
AAK19619.1	AF336286	Gossypium hirsutum	GHMYB9. ghmyb9. similar to myb.
CAA64614.1	X95296	Lycopersicon esculentum	transcription factor. THM27. myb-related.
CAA50224.1	X70879	Hordeum vulgare	MybHv1. myb1.

CAA50222.1	X70877	Hordeum vulgare	MybHv1. myb1.
AAA33067.1	L04497	Gossypium hirsutum	MYB A; putative.
CAA50221.1	X70876	Hordeum vulgare	MybHv5. myb2.
BAA23337.1	D88617	Oryza sativa	transfactor. OSMYB1. Osmyb1.
BAA23338.1	D88618	Oryza sativa	transfactor. OSMYB2. Osmyb2.
AAC04720.1	AF034134	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-O. similar to MYB A encoded by GenBank Accession Number L04497.
CAA72218.1	Y11415	Oryza sativa	myb.
CAA50225.1	X70880	Hordeum vulgare	MybHv5. myb2.
AAA82943.1	U39448	Picea mariana	MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the maize C1.
CAA78386.1	Z13996	Petunia x hybrida	DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
BAA81732.1	AB029161	Glycine max	GmMYB29A2.
AAK19616.1	AF336283	Gossypium hirsutum	GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.
AAK19611.1	AF336278	Gossypium hirsutum	BNLGH1233. bnlghi6233. similar to myb.
AAK19617.1	AF336284	Gossypium hirsutum	GHMYB36. ghmyb36. similar to myb.
BAA93038.1	AP001552	Oryza sativa	EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).
AAK19615.1	AF336282	Gossypium hirsutum	GHMYB10. ghmyb10. similar to myb.
BAB39987.1	AP003020	Oryza sativa	putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
BAB39972.1	AP003018	Oryza sativa	putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).

CAB43399.1	AJ006292	Antirrhinum majus	Myb-related transcription factor mixta-like 1. mybml1.
CAA72185.1	Y11350	Oryza sativa	myb factor. myb.
AAF22256.1	AF161711	Pimpinella brachycarpa	myb-related transcription factor.
AAG13574.1	AC037425	Oryza sativa	myb factor. OSJNBa0055P24.4.
BAA81731.1	AB029160	Glycine max	GmMYB29A1.
BAA81730.1	AB029159	Glycine max	GmMYB29A1.
CAA72186.1	Y11351	Oryza sativa	myb factor. myb.
CAA67600.1	X99210	Lycopersicon esculentum	myb-related transcription factor. THM16.
CAA75509.1	Y15219	Oryza sativa subsp. indica	transcriptional activator. C1.
AAC04718.1	AF034132	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-J. similar to MYB A encoded by GenBank Accession Number L04497.
CAA78387.1	Z13997	Petunia x hybrida	DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
BAA81736.1	AB029165	Glycine max	GmMYB29B2.
AAK19618.1	AF336285	Gossypium hirsutum	GHMYB38. ghmyb38. similar to myb.
CAA72217.1	Y11414	Oryza sativa	myb.
AAC49394.1	U57002	Zea mays	P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the C-terminal.
AAA33500.1	M73028	Zea mays	myb-like transcription factor. P.
BAB20661.1	AP002871	Oryza sativa	putative myb-related protein P. P0475H04.31.
AAG36774.1	AF210616	Zea mays	P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.
BAA88222.1	AB028650	Nicotiana tabacum	myb-related transcription factor LBM2. lbm2.
BAA81733.2	AB029162	Glycine max	GmMYB29A2.

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BAA23339.1 D88619 *Oryza sativa*  
transfactor. OSMYB3. Osmbyb3.

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BAA88224.1 AB028652 *Nicotiana tabacum*  
myb-related transcription factor LBM4. lbm4.

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BAA88221.1 AB028649 *Nicotiana tabacum*  
myb-related transcription factor LBM1. lbm1.

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AAB41101.1 U72762 *Nicotiana tabacum*  
transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.

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## SEQ ID NO: 536

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CAA70968.1 Y09825 *Solanum tuberosum*  
amino acid transporter. AAP1. transmembrane protein.

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AAF15946.1 AF061436 *Vicia faba*  
amino acid transporter c. AAPC.

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CAA70969.1 Y09826 *Solanum tuberosum*  
amino acid transporter. AAP2. transmembrane protein.

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AAB96830.1 U64823 *Nicotiana sylvestris*  
amino acid transporter. amino acid permease. nsaap1.

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CAA07563.1 AJ007574 *Ricinus communis*  
amino acid carrier. aap1.

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AAB48944.1 U31932 *Nicotiana sylvestris*  
amino acid permease 1. NSAAP1. amino acid transporter; Method: conceptual translation supplied by author.

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AAD16015.1 AF080544 *Nepenthes alata*  
amino acid transporter. AAP3.

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CAA70778.1 Y09591 *Vicia faba*  
amino acid transporter.

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AAF15944.1 AF061434 *Vicia faba*  
amino acid transporter a. AAPA.

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AAF15945.1 AF061435 *Vicia faba*  
amino acid transporter b. AAPB.

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AAF76897.1 AF274032 *Atriplex hortensis*  
proline/glycine betaine transporter.

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AAD16014.1 AF080543 *Nepenthes alata*  
amino acid transporter. AAP2.

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AAD25161.1 AF014809 *Lycopersicon esculentum*  
proline transporter 2. LeProT2.

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CAA10608.1 AJ132228 *Ricinus communis*  
amino acid carrier. aap3.

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## SEQ ID NO: 537

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BAA89009.1 AB027455 *Petunia x hybrida*  
anthocyanin 5-O-glucosyltransferase. PH1.

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BAA36423.1	AB013598	Verbena x hybrida	UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
BAA36421.1	AB013596	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.
BAB07962.1	AP002524	Oryza sativa	putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
BAA36422.1	AB013597	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.
BAA93039.1	AB033758	Citrus unshiu	limonoid UDP-glucosyltransferase. LGTase.
AAF61647.1	AF190634	Nicotiana tabacum	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
AAK16175.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.15.
AAF17077.1	AF199453	Sorghum bicolor	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
AAK16172.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.14.
BAA83484.1	AB031274	Scutellaria baicalensis	UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAK16181.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.16.
AAG25643.1	AF303396	Phaseolus vulgaris	UDP-glucosyltransferase HRA25. putative; defense associated.
AAK16178.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.5.
AAD21086.1	AF127218	Forsythia x intermedia	adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
BAA12737.1	D85186	Gentiana triflora	UDP-glucose:flavonoid-3-glucosyltransferase.
AAK28303.1	AF346431	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
CAB56231.1	Y18871	Dortheanthus bellidiformis	betanidin-5-O-glucosyltransferase.
CAA54612.1	X77462	Manihot esculenta	UTP-glucose glucosyltransferase. CGT5.

BAB41019.1	AB047092	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAB41020.1	AB047093	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
AAB36653.1	U32644	<i>Nicotiana tabacum</i>	immediate-early salicylate-induced glucosyltransferase. IS5a.
BAB41025.1	AB047098	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
BAB41023.1	AB047096	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
BAB41022.1	AB047095	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41021.1	AB047094	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAA19659.1	AB002818	<i>Perilla frutescens</i>	flavonoid 3-O-glucosyltransferase. UDP glucose.
BAB41026.1	AB047099	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
BAB41024.1	AB047097	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
AAK16180.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.21.
AAK28304.1	AF346432	<i>Nicotiana tabacum</i>	phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
AAB36652.1	U32643	<i>Nicotiana tabacum</i>	immediate-early salicylate-induced glucosyltransferase. IS10a.
BAB41017.1	AB047090	<i>Vitis labrusca</i> x <i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents <i>V. labruscana</i> cv. Ishiharawase.
BAA89008.1	AB027454	<i>Petunia</i> x <i>hybrida</i>	anthocyanidin 3-O-glucosyltransferase. PGT8.
CAA59450.1	X85138	<i>Lycopersicon esculentum</i>	twil. homologous to glucosyltransferases.
CAA54614.1	X77464	<i>Manihot esculenta</i>	UTP-glucose glucosyltransferase. CGT7.
CAA54611.1	X77461	<i>Manihot esculenta</i>	UTP-glucose glucosyltransferase. CGT2.
CAA54613.1	X77463	<i>Manihot esculenta</i>	UTP-glucose glucosyltransferase. CGT6.
SEQ ID NO: 540			
AAK27688.1	AF347614	<i>Lycopersicon esculentum</i>	sulfate transporter 2. ST2.

AAG41419.1	AF309643	Solanum tuberosum	high affinity sulfate transporter type 1. ST1.
AAK27687.1	AF347613	Lycopersicon esculentum	sulfate transporter 1. ST1.
AAA97952.1	U52867	Hordeum vulgare	high affinity sulfate transporter HVST1.
CAA57711.1	X82256	Stylosanthes hamata	high affinity sulphate transporter. SHST2.
CAA65291.1	X96431	Hordeum vulgare	high affinity sulphate transporter. HVST1.
CAA57710.1	X82255	Stylosanthes hamata	high affinity sulphate transporter. SHST1.
CAB42985.1	AJ238244	Aegilops tauschii	putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st1.
AAK35215.1	AF355602	Zea mays	sulfate transporter ST1.
CAB42986.1	AJ238245	Aegilops tauschii	putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st2.
CAA65536.1	X96761	Sporobolus stapfianus	sulphate transporter protein.
CAA57831.1	X82454	Stylosanthes hamata	low affinity sulphate transporter. SHST3.
CAA11413.1	AJ223495	Brassica juncea	sulfate permease. sp1.
AAB94543.1	AF016306	Zea mays	sulfate permease.
SEQ ID NO: 541			
AAF36491.1	AF129479	Hordeum vulgare	HAK2. HAK2. similar to Hordeum vulgare K+ transporter HAK1.
BAB32443.1	AB055630	Phragmites australis	high-affinity potassium transporter. PcnHAK1.
BAB32444.1	AB055631	Phragmites australis	high-affinity potassium transporter. PceHAK1A.
BAB32445.1	AB055632	Phragmites australis	high-affinity potassium transporter. PceHAK1B.
BAB32442.1	AB055629	Phragmites australis	high-affinity potassium transporter. PcuHAK1.
AAC39315.1	AF025292	Hordeum vulgare	putative high-affinity potassium transporter. HvHAK1.
AAF36497.1	AF129485	Oryza sativa	HAK4. HAK4. OsHAK4; similar to Hordeum vulgare K+ transporter HAK1.

AAF36496.1 AF129484 *Hordeum vulgare*  
HAK4. HAK4. HvHAK4; similar to *Hordeum vulgare* K<sup>+</sup> transporter HAK1.

CAC14883.1 AJ297888 *Hordeum vulgare*  
putative potassium transporter. hak1.

CAC14787.1 AJ297886 *Hordeum vulgare*  
putative potassium transporter. hak1.

AAF36492.1 AF129480 *Hordeum vulgare*  
HAK1B. HAK1B. HvHAK1B; similar to *Hordeum vulgare* K<sup>+</sup> transporter HAK1.

CAC15061.1 AJ300161 *Hordeum vulgare*  
potassium transporter. hak4.

SEQ ID NO: 542

AAA91063.1 M88254 *Hevea brasiliensis*  
ethylene-inducible protein. ER1.

SEQ ID NO: 546

CAA75386.1 Y15113 *Morinda citrifolia*  
3-deoxy-D-arabino-heptulosonate 7-phosphate synthase. DS3. 2-dehydro-3-deoxyphosphoheptonate aldolase.

CAA79855.1 Z21792 *Lycopersicon esculentum*  
phospho-2-dehydro-3-deoxyheptonate aldolase.

CAA79856.1 Z21793 *Lycopersicon esculentum*  
phospho-2-dehydro-3-deoxyheptonate aldolase.

SEQ ID NO: 548

BAA96751.1 AP002521 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome4, BAC clone T16H5; lectin like protein (AL024486).

SEQ ID NO: 551

BAB19096.1 AP002839 *Oryza sativa*  
putative DNA-binding protein homolog. P0688A04.2.

BAB19075.1 AP002744 *Oryza sativa*  
putative DNA-binding protein homolog. P0006C01.17.

AAK16170.1 AC079887 *Oryza sativa*  
putative DNA binding protein. OSJNBa0040E01.4.

AAD32677.1 AF140554 *Avena sativa*  
DNA-binding protein WRKY1. wrky1. putative transcription factor.

AAD16139.1 AF096299 *Nicotiana tabacum*  
DNA-binding protein 2. WRKY2. transcription factor.

CAB97004.1 AJ278507 *Solanum tuberosum*  
putative transcription factor. WRKY DNA binding protein. WRKY1.

CAA88326.1 Z48429 *Avena fatua*  
binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.

AAC49527.1 U48831 *Petroselinum crispum*  
WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.



AAC49529.1	U58540	Petroselinum crispum	WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
AAK16171.1	AC079887	Oryza sativa	putative DNA-binding protein. OSJNBa0040E01.10.
AAC37515.1	L44134	Cucumis sativus	SPF1-like DNA-binding protein.
AAD16138.1	AF096298	Nicotiana tabacum	DNA-binding protein 1. WRKY1. transcription factor.
AAD38283.1	AC007789	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAB18313.1	AP002865	Oryza sativa	putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
BAB40073.1	AP003074	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
AAC49528.1	U56834	Petroselinum crispum	DNA-binding. WRKY3. WRKY-type DNA-binding protein.
BAA77358.1	AB020023	Nicotiana tabacum	WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.
AAG46150.1	AC018727	Oryza sativa	putative DNA-binding protein. OSJNBa0056G17.18.
CAA88331.1	Z48431	Avena fatua	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAD32676.1	AF140553	Avena sativa	DNA-binding protein WRKY3. wrky3. putative transcription factor.
CAB66338.1	AJ279697	Betula pendula	wrky-type DNA binding protein. wrky.
AAF61863.1	AF193770	Nicotiana tabacum	DNA-binding protein 3. WRKY3. transcription factor.
AAF61864.1	AF193771	Nicotiana tabacum	DNA-binding protein 4. WRKY4. transcription factor.
AAD27591.1	AF121354	Petroselinum crispum	binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.
BAA87069.1	AB035271	Matricaria chamomilla	elicitor-induced DNA-binding protein homolog. McWRKY1.
SEQ ID NO: 553			
AAF34428.1	AF172282	Oryza sativa	receptor-like protein kinase. DUPR11.18.
BAA94518.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
BAB07904.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.12.

BAA94516.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07906.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.14.
BAA94517.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
BAA94528.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).
BAA94529.2	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.

AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
SEQ ID NO: 554			
CAC05658.1	AJ250919	Brassica napus	endopolygalacturonase. pegaz.
CAC05657.1	AJ250918	Brassica napus	endopolygalacturonase. pgaz.
CAA65072.1	X95800	Brassica napus	polygalacturonase.
CAA90272.1	Z49971	Brassica napus	Hydrolytic enzyme. Polygalacturonase. pga.
CAA54448.1	X77231	Prunus persica	polygalacturonase. PG.
AAC14453.1	L12019	Actinidia deliciosa	polygalacturonase.
AAF71160.1	AF152758	Actinidia chinensis	polygalacturonase A. PGA.
AAA34178.1	M37304	Lycopersicon esculentum	polygalacturonase.
CAA32235.1	X14074	Lycopersicon esculentum	polygalacturonase.
CAA29148.1	X05656	Lycopersicon esculentum	polygalacturonase (AA 1-457).
AAA32914.1	L06094	Persea americana	cell wall degradation. polygalacturonase.
CAA47055.1	X66426	Persea americana	polygalacturonase.
AAC26512.1	AF062467	Cucumis melo	polygalacturonase precursor. MPG3.
CAA11846.1	AJ224147	Rubus idaeus	polygalacturonase. RAS3.
AAF61444.1	AF138858	Lycopersicon esculentum	hydrolyses polygalacturonic acid. polygalacturonase. XOPG1.
BAA88472.1	AB035890	Cucumis sativus	polygalacturonase. CUPG1.
AAD46483.1	AF128266	Glycine max	polygalacturonase PG1.
AAD46484.1	AF128267	Glycine max	polygalacturonase PG2.

AAC28905.1	AF001002	<i>Lycopersicon esculentum</i> hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 4. TAPG4. expressed in abscission.
AAC28906.1	AF001003	<i>Lycopersicon esculentum</i> hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 5. TAPG5. expressed in abscission.
AAC28903.1	AF001000	<i>Lycopersicon esculentum</i> hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 1. TAPG1. expressed in abscission.
AAA80489.1	U23053	<i>Lycopersicon esculentum</i> polygalacturonase precursor.
AAC64184.1	AF095577	<i>Prunus persica</i> endopolygalacturonase.
AAC28902.2	AF000999	<i>Lycopersicon esculentum</i> hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 3. TAPG3. expressed in abscission.
AAB09575.1	U70480	<i>Lycopersicon esculentum</i> abscission polygalacturonase. TAPG2.
AAC28904.1	AF001001	<i>Lycopersicon esculentum</i> hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 2. TAPG2. expressed in abscission.
CAA54150.1	X76735	<i>Prunus persica</i> endopolygalacturonase.
AAC70951.1	AF072732	<i>Lycopersicon esculentum</i> hydrolyzes pectin in the cell wall and middle lamella. polygalacturonase 7. specifically and abundantly expressed in pistils.
AAC26511.1	AF062466	<i>Cucumis melo</i> polygalacturonase precursor. MPG2.
AAB09576.1	U70481	<i>Lycopersicon esculentum</i> abscission polygalacturonase. TAPG4.
AAC28947.1	AF029230	<i>Lycopersicon esculentum</i> polygalacturonase. TPG6.
AAA82167.1	U09717	<i>Gossypium hirsutum</i> polygalacturonase.
AAA58322.1	U09805	<i>Gossypium barbadense</i> polygalacturonase.
CAA47052.1	X66422	<i>Zea mays</i> polygalacturonase. PG.
AAG14416.1	AF248538	<i>Nicotiana tabacum</i> NTS1 protein. similar to polygalacturonase.
CAB42886.1	AJ238848	<i>Phleum pratense</i> polygalacturonase. pg.

CAA40850.1	X57627	Zea mays	polygalacturonase.
CAA46679.1	X65844	Zea mays	polygalacturonase. PGg6.
CAA40910.1	X57743	Zea mays	polygalacturonase.
CAA44249.1	X62385	Zea mays	polygalacturonase.
CAA45751.1	X64408	Zea mays	polygalacturonase. PG. pollen-preferentially expressed.
CAA40851.1	X57628	Zea mays	polygalacturonase.
CAA46680.1	X65845	Zea mays	polygalacturonase. PGg14.
AAC26510.1	AF062465	Cucumis melo	polygalacturonase precursor. MPG1.
SEQ ID NO: 556			
CAA51734.1	X73301	Vigna mungo	alpha-amylase. amyVm1.
CAA37217.1	X53049	Vigna mungo	alpha-amylase (AA 1-421).
BAA33879.1	AB015131	Phaseolus vulgaris	alpha-amylase.
AAA16513.1	U06754	Cuscuta reflexa	starch hydrolysis. alpha amylase precursor. CUS AMY2.
AAA98615.1	J04202	Hordeum vulgare	alpha-amylase. Amy46. precursor.
AAA98790.1	K02637	Hordeum vulgare	alpha-amylase type B. Amy6-4. precursor.
CAA33298.1	X15226	Hordeum vulgare	alpha-amylase.
AAA33885.1	M24286	Oryza sativa	alpha-amylase (EC 3.2.1.1).
CAA34516.1	X16509	Oryza sativa	alpha-amylase.
CAA72144.1	Y11277	Hordeum vulgare	alpha-amylase. amy.
CAA33299.1	X15227	Hordeum vulgare	alpha amylase.
AAA32925.1	M17126	Hordeum vulgare	alpha-amylase 1.

AAA32927.1	M17128	Hordeum vulgare alpha-amylase 2.
AAA32929.1	J01236	Hordeum vulgare alpha-amylase type A, EC 3.2.1.1.
CAA39777.1	X56337	Oryza sativa alpha-amylase. RAmy3B.
CAA09323.1	AJ010728	Avena fatua alpha amylase. alpha-Amy2A.
AAA33897.1	M24941	Oryza sativa alpha-amylase precursor (EC 3.2.1.1).
CAA09324.1	AJ010729	Avena fatua alpha-amylase. alpha-Amy2D.
CAA28803.1	X05166	Hordeum vulgare alpha-amylase type A. Amy32b.
AAA32926.1	M17125	Hordeum vulgare alpha-amylase 1.
CAA39778.1	X56338	Oryza sativa alpha-amylase. RAmy3C.
AAA32935.1	M15208	Hordeum vulgare alpha-amylase.
AAA33895.1	M59351	Oryza sativa alpha-amylase. RAmy3D.
AAA33896.1	M59352	Oryza sativa alpha-amylase. RAmy3E.
AAA50161.1	L25805	Zea mays alpha-amylase.
AAA33894.1	M74177	Oryza sativa alpha-amylase. amy2A.
CAA72143.1	Y11276	Hordeum vulgare alpha-amylase. amy.
CAA39776.1	X56336	Oryza sativa alpha-amylase. RAmy3A.
CAA45903.1	X64619	Oryza sativa alpha-amylase. Amyc2. starts hydrolysis during seed germination.
AAA33886.1	M24287	Oryza sativa alpha-amylase (EC 3.2.1.1).
AAA32928.1	M17127	Hordeum vulgare alpha-amylase 2.
AAA32933.1	K02638	Hordeum vulgare pre-alpha-amylase type B, EC 3.2.1.1.
AAA91883.1	M81682	Solanum tuberosum alpha-amylase. Amy23.

AAA34259.1	M16991	Triticum aestivum alpha-amylase.
CAA29252.1	X05809	Triticum aestivum alpha-amylase.
AAA91884.1	M79328	Solanum tuberosum alpha-amylase.
AAF63239.1	AF153828	Malus x domestica degrades starch. alpha-amylase. alpha-amylase by similarity.
AAA32930.1	M10056	Hordeum vulgare alpha-amylase type B, EC 3.2.1.1.
AAA32931.1	K02635	Hordeum vulgare alpha-amylase type B, EC 3.2.1.1.
CAA36485.1	X52240	Oryza sativa alpha-amylase. OSamy-c.
AAA32932.1	K02636	Hordeum vulgare alpha-amylase type B, EC 3.2.1.1.
SEQ ID NO: 557		
CAA90272.1	Z49971	Brassica napus Hydrolytic enzyme. Polygalacturonase. pga.
CAA65072.1	X95800	Brassica napus polygalacturonase.
CAA67020.1	X98373	Brassica napus endo-polygalacturonidase.
CAC05658.1	AJ250919	Brassica napus endopolygalacturonase. pegaz.
CAC05657.1	AJ250918	Brassica napus endopolygalacturonase. pgaz.
AAC14453.1	L12019	Actinidia deliciosa polygalacturonase.
AAF71160.1	AF152758	Actinidia chinensis polygalacturonase A. PGA.
CAA54448.1	X77231	Prunus persica polygalacturonase. PG.
AAA34178.1	M37304	Lycopersicon esculentum polygalacturonase.
CAA29148.1	X05656	Lycopersicon esculentum polygalacturonase (AA 1-457).
CAA32235.1	X14074	Lycopersicon esculentum polygalacturonase.
AAA32914.1	L06094	Persea americana cell wall degradation. polygalacturonase.

CAA47055.1	X66426	Persea americana	polygalacturonase.
AAC26512.1	AF062467	Cucumis melo	polygalacturonase precursor. MPG3.
CAA11846.1	AJ224147	Rubus idaeus	polygalacturonase. RAS3.
BAA88472.1	AB035890	Cucumis sativus	polygalacturonase. CUPG1.
AAF61444.1	AF138858	Lycopersicon esculentum	hydrolyses polygalacturonic acid. polygalacturonase. XOPG1.
AAA80489.1	U23053	Lycopersicon esculentum	polygalacturonase precursor.
AAC28903.1	AF001000	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 1. TAPG1. expressed in abscission.
AAB09575.1	U70480	Lycopersicon esculentum	abscission polygalacturonase. TAPG2.
AAC28904.1	AF001001	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 2. TAPG2. expressed in abscission.
AAC28905.1	AF001002	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 4. TAPG4. expressed in abscission.
AAC64184.1	AF095577	Prunus persica	endopolygalacturonase.
AAD46483.1	AF128266	Glycine max	polygalacturonase PG1.
AAC28906.1	AF001003	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 5. TAPG5. expressed in abscission.
AAD46484.1	AF128267	Glycine max	polygalacturonase PG2.
CAA54150.1	X76735	Prunus persica	endopolygalacturonase.
AAC26511.1	AF062466	Cucumis melo	polygalacturonase precursor. MPG2.
AAC28902.2	AF000999	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 3. TAPG3. expressed in abscission.
AAC70951.1	AF072732	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella. polygalacturonase 7. specifically and abundantly expressed in pistils.



CAA47052.1	X66422	Zea mays	polygalacturonase. PG.
AAC28947.1	AF029230	Lycopersicon esculentum	polygalacturonase. TPG6.
AAA82167.1	U09717	Gossypium hirsutum	polygalacturonase.
AAB09576.1	U70481	Lycopersicon esculentum	abscission polygalacturonase. TAPG4.
CAA40910.1	X57743	Zea mays	polygalacturonase.
CAA44249.1	X62385	Zea mays	polygalacturonase.
CAA40850.1	X57627	Zea mays	polygalacturonase.
AAG14416.1	AF248538	Nicotiana tabacum	NTS1 protein. similar to polygalacturonase.
CAA46679.1	X65844	Zea mays	polygalacturonase. PGg6.
AAC26510.1	AF062465	Cucumis melo	polygalacturonase precursor. MPG1.
AAA58322.1	U09805	Gossypium barbadense	polygalacturonase.
CAA46680.1	X65845	Zea mays	polygalacturonase. PGg14.
CAA40851.1	X57628	Zea mays	polygalacturonase.
CAA45751.1	X64408	Zea mays	polygalacturonase. PG. pollen-preferentially expressed.
CAB42886.1	AJ238848	Phleum pratense	polygalacturonase. pg.
SEQ ID NO: 559			
CAB43937.1	AJ006348	Fragaria x ananassa	cell wall hydrolysis. endo-beta-1,4-glucanase. eg1.
AAC95009.1	AF074923	Fragaria x ananassa	endo-1,4-beta-glucanase precursor. Cell1. 1,4-beta-glucanohydrolase.
AAC12684.1	U76725	Pinus radiata	endo-beta-1,4-glucanase. PrCell1. cellulase; PRCEL1.
AAA69909.1	U13055	Lycopersicon esculentum	cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel2. cellulase.
CAA65600.1	X96856	Prunus persica	endo-beta-1,4-glucanase. ppEG1.

CAA65597.1	X96853	Prunus persica	endo-beta-1,4-glucanase. pcel1.
CAA65827.1	X97189	Capsicum annuum	endo-beta-1,4-glucanase. ccel3. cellulase.
AAC62241.1	AF077339	Lycopersicon esculentum	endo-1,4-beta-glucanase. cel5. cellulase; also expressed in fruit and pistils.
BAA85150.1	AB032830	Pisum sativum	endo-1,4-beta-glucanase. EGL2.
AAA80495.1	U20590	Lycopersicon esculentum	endo-1,4-beta-glucanase precursor. cellulase.
BAB32662.1	AB055886	Atriplex lentiformis	beta-1,4-glucanase. Al-cell1. cellulase.
CAA65828.1	X97190	Capsicum annuum	endo-beta-1,4-glucanase. ccel2.
AAC12685.1	U76756	Pinus radiata	endo-beta-1,4-glucanase. PrCel2. cellulase; PRCEL2.
BAA77239.1	AB025796	Populus alba	endo-1,4-beta glucanase. POPCEL2. cellulase.
CAB59900.1	AJ010950	Capsicum annuum	cell wall degradation. endo-beta-1,4-glucanase. eg2.
BAB39483.1	AB049200	Populus alba	endo-1,4-beta-glucanase. PopCel2.
BAB39482.1	AB049199	Populus alba	endo-1,4-beta glucanase. PopCell1.
CAA72133.1	Y11268	Lycopersicon esculentum	endo-1,4-beta-D-glucanase. cel7.
AAA96135.1	L41046	Pisum sativum	endo-1,4-beta-glucanase. EGL1.
AAC78504.1	U34754	Phaseolus vulgaris	endo-1,4-beta-D-glucanase. cellulase.
AAA02563.1	M57400	Phaseolus vulgaris	cellulase precursor. endo-1,4-beta-D-glucanase.
CAA60737.1	X87323	Capsicum annuum	catalyzes hydrolysis of cell wall polysaccharides. cellulase. cel1. Beta-1,4-endoglycanohydrolase.
CAA65826.1	X97188	Capsicum annuum	endo-beta-1,4-glucanase. ccel1. cellulase.
AAA69908.1	U13054	Lycopersicon esculentum	cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel1. cellulase.
CAB43938.1	AJ006349	Fragaria x ananassa	cell wall hydrolysis. endo-beta-1,4-glucanase. eg3.

BAA96209.1	AP002094	Oryza sativa	EST C72268(E1328) corresponds to a region of the predicted gene. Similar to <i>Fragaria x ananassa</i> endo-beta-1,4-glucanase (AJ006349).
BAA96207.1	AP002094	Oryza sativa	EST C72268(E1328) corresponds to a region of the predicted gene. Similar to <i>Fragaria x ananassa</i> endo-beta-1,4-glucanase (AJ006349).
AAD08699.1	AF098292	Lycopersicon esculentum	endo-beta-1,4-D-glucanase. Cel8.
BAA94257.1	AB040769	Hordeum vulgare	endo-1,4-beta-glucanase Cell. Cell1.
AAC49704.1	U78526	Lycopersicon esculentum	endo-1,4-beta-glucanase. Cel3.
CAB51903.1	AJ242807	Brassica napus	endo-1,4-beta-D-glucanase. Cell16. cellulase.
AAA20082.1	U00730	Glycine max	CMCase; cellulase; endo-1,4-beta-D-glucanase.
CAA11301.1	AJ223386	Fragaria x ananassa	endo-beta-1,4-glucanase. faEG1. partial cDNA obtained by RT-PCR amplification.
CAA11302.1	AJ223387	Fragaria x ananassa	endo-beta-1,4-glucanase. partial cDNA obtained by RT-PCR amplification.
BAA21111.1	D88417	Gossypium hirsutum	endo-1,4-beta-glucanase.
AAA20083.1	U00731	Glycine max	CMCase; cellulase; endo-1,4-beta-D-glucanase.
SEQ ID NO: 560			
AAB97617.1	U83687	Apium graveolens	NADPH-dependent mannose 6-phosphate reductase. m6pr. aldo-keto reductase; similar to aldose 6-phosphate reductase also known as NADP-sorbitol-6-phosphate dehydrogenase encoded by GenBank Accession Number D11080.
AAC97607.1	AF057134	Malus x domestica	synthesizes sorbitol, a major photosynthetic product in many members of the Rosaceae family. NADP-dependent sorbitol 6-phosphate dehydrogenase. S6PDH.
BAA01853.1	D11080	Malus x domestica	NADP-dependent D-sorbitol-6-phosphate dehydrogenase. S6PDH.
SEQ ID NO: 561			
CAB43938.1	AJ006349	Fragaria x ananassa	cell wall hydrolysis. endo-beta-1,4-glucanase. eg3.
BAA96209.1	AP002094	Oryza sativa	EST C72268(E1328) corresponds to a region of the predicted gene. Similar to <i>Fragaria x ananassa</i> endo-beta-1,4-glucanase (AJ006349).
BAA96207.1	AP002094	Oryza sativa	EST C72268(E1328) corresponds to a region of the predicted gene. Similar to <i>Fragaria x ananassa</i> endo-beta-1,4-glucanase (AJ006349).

AAD08699.1	AF098292	<i>Lycopersicon esculentum</i> endo-beta-1,4-D-glucanase. Cel8.
BAA21111.1	D88417	<i>Gossypium hirsutum</i> endo-1,4-beta-glucanase.
CAA65828.1	X97190	<i>Capsicum annuum</i> endo-beta-1,4-glucanase. ccel2.
CAB59900.1	AJ010950	<i>Capsicum annuum</i> cell wall degradation. endo-beta-1,4-glucanase. eg2.
AAC95009.1	AF074923	<i>Fragaria x ananassa</i> endo-1,4-beta-glucanase precursor. Cel1. 1,4-beta-glucanohydrolase.
CAB43937.1	AJ006348	<i>Fragaria x ananassa</i> cell wall hydrolysis. endo-beta-1,4-glucanase. eg1.
AAA80495.1	U20590	<i>Lycopersicon esculentum</i> endo-1,4-beta-glucanase precursor. cellulase.
BAA85150.1	AB032830	<i>Pisum sativum</i> endo-1,4-beta-glucanase. EGL2.
AAC12684.1	U76725	<i>Pinus radiata</i> endo-beta-1,4-glucanase. PrCell. cellulase; PRCEL1.
BAB32662.1	AB055886	<i>Atriplex lentiformis</i> beta-1,4-glucanase. Al-cell. cellulase.
AAC62241.1	AF077339	<i>Lycopersicon esculentum</i> endo-1,4-beta-glucanase. cel5. cellulase; also expressed in fruit and pistils.
CAA65826.1	X97188	<i>Capsicum annuum</i> endo-beta-1,4-glucanase. ccell1. cellulase.
AAA69909.1	U13055	<i>Lycopersicon esculentum</i> cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel2. cellulase.
CAA65597.1	X96853	<i>Prunus persica</i> endo-beta-1,4-glucanase. pcell1.
CAA65600.1	X96856	<i>Prunus persica</i> endo-beta-1,4-glucanase. ppEG1.
AAC12685.1	U76756	<i>Pinus radiata</i> endo-beta-1,4-glucanase. PrCel2. cellulase; PRCEL2.
BAB39482.1	AB049199	<i>Populus alba</i> endo-1,4-beta glucanase. PopCell1.
CAA65827.1	X97189	<i>Capsicum annuum</i> endo-beta-1,4-glucanase. ccel3. cellulase.
BAB39483.1	AB049200	<i>Populus alba</i> endo-1,4-beta-glucanase. PopCel2.
BAA77239.1	AB025796	<i>Populus alba</i> endo-1,4-beta glucanase. POPCEL2. cellulase.
AAA69908.1	U13054	<i>Lycopersicon esculentum</i> cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel1. cellulase.

AAC78504.1	U34754	Phaseolus vulgaris	endo-1,4-beta-D-glucanase. cellulase.
AAA02563.1	M57400	Phaseolus vulgaris	cellulase precursor. endo-1,4-beta-D-glucanase.
CAA72133.1	Y11268	Lycopersicon esculentum	endo-1,4-beta-D-glucanase. cel7.
AAA96135.1	L41046	Pisum sativum	endo-1,4-beta-glucanase. EGL1.
CAB51903.1	AJ242807	Brassica napus	endo-1,4-beta-D-glucanase. Cell16. cellulase.
AAC49704.1	U78526	Lycopersicon esculentum	endo-1,4-beta-glucanase. Cel3.
BAA94257.1	AB040769	Hordeum vulgare	endo-1,4-beta-glucanase Cell1. Cell1.
CAA11302.1	AJ223387	Fragaria x ananassa	endo-beta-1,4-glucanase. partial cDNA obtained by RT-PCR amplification.
AAA20082.1	U00730	Glycine max	CMCase; cellulase; endo-1,4-beta-D-glucanase.
CAA11301.1	AJ223386	Fragaria x ananassa	endo-beta-1,4-glucanase. faEG1. partial cDNA obtained by RT-PCR amplification.
AAC64045.1	AF077340	Lycopersicon esculentum	endo-1,4-beta-glucanase. cel5. cellulase.
SEQ ID NO: 562			
AAD53011.1	AF089848	Brassica napus	senescence-specific cysteine protease. SAG12-1. BnSAG12-1.
AAD53012.1	AF089849	Brassica napus	senescence-specific cysteine protease. SAG12-2. BnSAG12-2.
AAK27968.1	AF242372	Ipomoea batatas	cysteine protease. SPCP1.
AAA50755.1	U13940	Alnus glutinosa	cysteine proteinase. putative preproprotein.
BAB13759.1	AB040454	Astragalus sinicus	cysteine proteinase. AsNODf32. preproprotein putative.
AAC62396.1	AF050756	Ricinus communis	cysteine endopeptidase precursor. CysEP.
CAB09698.1	Z97022	Hordeum vulgare	cysteine proteinase. putative.
CAA52425.1	X74406	Hemerocallis sp.	thiol-protease. SEN102.
BAA83472.1	AB004648	Oryza sativa	cysteine endopeptidase. RepA.

CAA56844.1	X80876	Oryza sativa	cysteine protease.
BAA88898.1	AB020961	Zea mays	cysteine protease component of protease-inhibitor complex. CPPIC.
AAC35211.1	U12637	Hemerocallis hybrid cultivar	cysteine proteinase. SEN11.
CAB09697.1	Z97021	Hordeum vulgare	cysteine endopeptidase EP-A. precursor.
AAB88263.1	AF019147	Zea mays	cysteine proteinase Mir3. mir3.
AAD28477.1	AF133839	Sandersonia aurantiaca	papain-like cysteine protease. PRT5. senescence-related.
CAB16317.1	Z99173	Nicotiana tabacum	storage protein hydrolysis. cysteine proteinase precursor.
CAB09699.1	Z97023	Hordeum vulgare	cysteine endopeptidase EP-A.
AAD10337.1	U94591	Hordeum vulgare	cysteine proteinase precursor. EPA.
CAA06243.1	AJ004958	Pisum sativum	thiol-protease. pre-pro-TPE4A protein. tpE4A.
CAB53515.1	AJ245924	Solanum tuberosum	proteolysis. cysteine protease. cyp.
AAD48496.1	AF172856	Lycopersicon esculentum	cysteine protease TDI-65. tdi-65. induced by drought; localized in the nuclei and chloroplast (Tabaeizadeh, Z. et al., 1995. Protoplasma, 186:208-219).
CAA05894.1	AJ003137	Lycopersicon esculentum	cysteine protease. CYP1. C14.
AAA79915.1	U17135	Dianthus caryophyllus	cysteine proteinase. DCCP1. expressed in senescing flower petals.
AAB37233.1	U34747	Phalaenopsis sp. SM9108	cysteine proteinase.
CAB17076.1	Z99954	Phaseolus vulgaris	protein hydrolysis. cysteine proteinase precursor.
CAA84378.1	Z34895	Vicia sativa	storage protein degradation. cysteine proteinase.
CAA53377.1	X75749	Vicia sativa	storage protein hydrolysis. cysteine protease.
CAB17074.1	Z99952	Phaseolus vulgaris	degradation of storage proteins. cysteine proteinase precursor.
AAB68374.1	U52970	Phaseolus vulgaris	suggested to initiate phaseolin degradation during germination. cysteine endopeptidase 1. PvCEP-1.

CAA12118.1	AJ224766	Phaseolus vulgaris	phaseolin degradation. cysteine protease.
AAC49455.1	U41902	Pseudotsuga menziesii	cysteine protease. Pseudotsugain. PM33cysP.
CAA46863.1	X66061	Pisum sativum	thiolprotease. tpp. start codon ttg.
AAB41816.1	U44947	Pisum sativum	NTH1. PsCyp1. cysteine protease homolog.
BAA83473.1	AB004819	Oryza sativa	cysteine endopeptidase. Rep1.
BAA22544.1	D38532	Ananas comosus	precursor of cysteine proteinase. FBSB precursor. stem bromelain precursor in fruit.
BAA11170.1	D76415	Oryza sativa	cysteine proteinase.
AAD20453.1	AF099203	Oryza sativa	cysteine endopeptidase precursor. EP3A.
CAA08860.1	AJ009829	Ananas comosus	cysteine proteinase precursor, AN8. an8.
AAA85036.1	U19384	Hordeum vulgare	cysteine proteinase EPB2 precursor.
AAA85035.1	U19359	Hordeum vulgare	cysteine proteinase EPB1 precursor.
SEQ ID NO: 565			
AAA97411.1	U51918	Pisum sativum	pyruvate dehydrogenase E1 alpha subunit.
CAA81558.1	Z26949	Solanum tuberosum	subunit of the mitochondrial pyruvate dehydrogenase complex. E1 alpha subunit of pyruvate dehydrogenase precursor.
AAC72195.1	AF069911	Zea mays	pyruvate dehydrogenase E1 alpha subunit.
AAG43499.1	AF209924	Lycopersicon esculentum	pyruvate dehydrogenase.
CAB08111.1	Z94180	Lycopersicon esculentum	branched chain alpha-keto acid dehydrogenase E1-alpha subunit.
SEQ ID NO: 566			
AAD55090.1	AF178653	Vitis riparia	thaumatin. osmotin; pathogenesis-related protein.
CAA51432.1	X72928	Solanum commersonii	osmotin-like protein.
CAA47601.1	X67121	Solanum commersonii	osmotin-like protein.
CAC34055.1	AJ297410	Capsicum annuum	osmotin-like protein. pr5 p23.

CAA47047.1	X66416	Lycopersicon esculentum	tpm 1. Induced during viroid infection. Osmotin-like, antifungal protein homologue.
AAB23375.1	S44889	Nicotiana tabacum	osmotin. osmotin. pathogenesis-related protein homolog; This sequence comes from Fig. 3.
AAB22459.2	S40046	Nicotiana tabacum	osmotin. abscisic acid-activated. basic PR-like protein; This sequence comes from Fig. 1A; conceptual translation presented here differs from translation in publication; mismatch(181[R->G]).
AAG16625.1	AY007309	Solanum dulcamara	cryoprotective osmotin-like protein.
CAA46623.1	X65701	Nicotiana tabacum	osmotin. AP24.
CAA46622.1	X65700	Nicotiana tabacum	osmotin. AP24.
CAA51431.1	X72927	Solanum commersonii	osmotin-like protein.
CAA64620.1	X95308	Nicotiana tabacum	PR protein. osmotin.
CAA51430.1	X72926	Solanum commersonii	osmotin-like protein.
AAC64171.1	AF093743	Lycopersicon esculentum	pathogenesis-related protein osmotin precursor. NP24.
AAB61590.1	AF003007	Vitis vinifera	VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.
BAA11180.1	D76437	Nicotiana sylvestris	antifungal activity. neutral PR-5 (osmotin-like protein, PR-5d). neutral isoform of pathogenesis-related protein group 5.
AAA34087.1	M64081	Nicotiana tabacum	osmotin-like protein. OLP1.
CAA47669.1	X67244	Solanum commersonii	osmotin-like protein.
CAA71883.1	Y10992	Vitis vinifera	osmotin-like protein. OSM1.
AAF13707.1	AF199508	Fragaria x ananassa	osmotin-like protein. olp.
AAA34089.1	M29279	Nicotiana tabacum	osmotin.
CAA43854.1	X61679	Nicotiana tabacum	osmotin.
CAA04642.1	AJ001268	Hordeum vulgare	antifungal. basic pathogenesis-related protein PR5. osmotin/permatin-like.
CAC22330.1	AJ298304	Fagus sylvatica	stress protein. osmotin-like protein. olp2.



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CAC22329.1 AJ298303 *Fagus sylvatica*  
stress protein. osmotin-like protein. olp.

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AAB67852.1 L76377 *Oryza sativa*  
osmotin. 14b.

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CAB36911.1 AJ000692 *Quercus suber*  
stress protein. osmotin-like protein. olp.

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SEQ ID NO: 569

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BAA95814.1 AP002069 *Oryza sativa*  
ESTs AU082579(S2069),D40238(S2069) correspond to a region of the predicted gene.  
Similar to *Arabidopsis thaliana* vesicle-associated membrane protein 7C; synaptobrevin 7C.  
(AF025332).

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SEQ ID NO: 572

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AAA92677.1 U13736 *Pisum sativum*  
binds calcium. calmodulin-like protein.

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AAA34015.1 L01433 *Glycine max*  
calcium-binding regulatory protein. calmodulin. SCaM-4. putative.

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AAA33948.1 L19359 *Glycine max*  
calcium-binding regulatory protein. calmodulin. SCaM-5. putative.

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CAA66159.1 X97558 *Capsicum annuum*  
calmodulin-1.

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CAA09302.1 AJ010645 *Capsicum annuum*  
calcium binding protein. calmodulin 3 protein. calmodulin 3.

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AAA34144.1 M67472 *Lycopersicon esculentum*  
calmodulin. CALM1LE.

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CAA62150.1 X90560 *Physcomitrella patens*  
Calmodulin. CaM.

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AAB46588.1 U83402 *Capsicum annuum*  
calmodulin.

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BAA87825.1 AP000815 *Oryza sativa*  
ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene.  
Similar to *O.sativa* gene encoding calmodulin. (Z12828).

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AAF65511.1 AF108889 *Capsicum annuum*  
calmodulin.

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AAA85157.1 U20297 *Solanum tuberosum*  
calcium-binding protein. calmodulin.

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AAA85156.1 U20296 *Solanum tuberosum*  
calcium-binding protein. calmodulin.

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AAA62351.1 U20295 *Solanum tuberosum*  
calcium-binding protein. calmodulin.

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AAA85155.1 U20294 *Solanum tuberosum*  
calcium-binding protein. calmodulin.

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AAA33900.1 L18914 *Oryza sativa*  
calcium binding protein, signal transduction. calmodulin.

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CAA78288.1	Z12828	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
AAC49583.1	U48692	Triticum aestivum	calmodulin TaCaM2-3. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum	calmodulin TaCaM2-2. calcium-binding protein.
CAA61980.1	X89890	Bidens pilosa	Calmodulin.
CAA67054.1	X98404	Capsicum annuum	calmodulin-2.
AAA33083.1	M20729	Chlamydomonas reinhardtii	calmodulin.
AAG11418.1	AF292108	Prunus avium	calmodulin.
AAF33852.1	AF231026	Oryza sativa	calmodulin-like protein.
AAA92681.1	U13882	Pisum sativum	calcium-binding protein. calmodulin.
AAA33706.1	M80836	Petunia x hybrida	calmodulin. CAM81.
AAA33705.1	M80831	Petunia x hybrida	calmodulin-related protein. CAM53.
AAA98933.1	U37936	Oryza sativa	novel calmodulin-like protein. C-terminal of this sequence contains a CAAX box which is common in signal transport protein, but not in calmodulin.
CAA43143.1	X60738	Malus x domestica	Calmodulin. CaM.
CAA78301.1	Z12839	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin. putative.
CAA42423.1	X59751	Daucus carota	calmodulin. Ccam-1.
AAF73157.1	AF150059	Brassica napus	calmodulin. CaM1. involved in seed germination.
AAA19571.1	U10150	Brassica napus	calcium binding. calmodulin. bcm1.
AAA87347.1	M88307	Brassica juncea	calmodulin.
AAG27432.1	AF295637	Elaeis guineensis	calmodulin.
BAA94697.1	AB041712	Chara corallina	calmodulin. cccam2.

BAA94696.1	AB041711	Chara corallina	calmodulin. cccam1.
BAA96536.1	AB044286	Chara corallina	calmodulin. ccam.
AAC18355.1	AF064456	Oryza sativa subsp. indica	calmodulin-like protein. CAM-like.
AAA34237.1	L20691	Vigna radiata	calmodulin.
CAA52602.1	X74490	Zea mays	Calmodulin. ZMCALM1.
CAA54583.1	X77397	Zea mays	calmodulin. CaM2.
AAC49585.1	U49103	Triticum aestivum	calmodulin TaCaM3-2. calcium-binding protein.
AAC49586.1	U49104	Triticum aestivum	calmodulin TaCaM3-3. calcium-binding protein.
AAC49587.1	U49105	Triticum aestivum	calmodulin TaCaM4-1. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum	calmodulin TaCaM1-3. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum	calmodulin TaCaM3-1. calcium-binding protein.
SEQ ID NO: 575			
AAK28303.1	AF346431	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
AAB36653.1	U32644	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS5a.
AAB36652.1	U32643	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
CAA59450.1	X85138	Lycopersicon esculentum	twil. homologous to glucosyltransferases.
CAB56231.1	Y18871	Dorotheanthus bellidiformis	betanidin-5-O-glucosyltransferase.
BAA83484.1	AB031274	Scutellaria baicalensis	UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAB48444.1	U82367	Solanum tuberosum	UDP-glucose glucosyltransferase.
CAA54610.1	X77460	Manihot esculenta	UTP-glucose glucosyltransferase. CGT4.

AAD04166.1	AF101972	Phaseolus lunatus	catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
BAB17182.1	AP002843	Oryza sativa	putative UTP-glucose glucosyltransferase. P0407B12.19.
BAA93039.1	AB033758	Citrus unshiu	limonoid UDP-glucosyltransferase. LGTase.
AAF61647.1	AF190634	Nicotiana tabacum	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAB17176.1	AP002843	Oryza sativa	putative UTP-glucose glucosyltransferase. P0407B12.13.
CAC09351.1	AL442007	Oryza sativa	putative glucosyltransferase. H0212B02.7.
CAA54611.1	X77461	Manihot esculenta	UTP-glucose glucosyltransferase. CGT2.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
AAK16181.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.16.
AAK16178.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.5.
CAA54612.1	X77462	Manihot esculenta	UTP-glucose glucosyltransferase. CGT5.
AAK16180.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.21.
AAF17077.1	AF199453	Sorghum bicolor	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
CAA54609.1	X77459	Manihot esculenta	UTP-glucose glucosyltransferase. CGT1.
BAB41025.1	AB047098	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
AAK16172.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.14.
BAB41019.1	AB047092	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAB41018.1	AB047091	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.

BAB41023.1	AB047096	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
BAB41021.1	AB047094	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAA89009.1	AB027455	Petunia x hybrida	anthocyanin 5-O-glucosyltransferase. PH1.
AAB81682.1	AF000371	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41017.1	AB047090	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
BAB41022.1	AB047095	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41020.1	AB047093	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
BAB41024.1	AB047097	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
AAB81683.1	AF000372	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41026.1	AB047099	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
CAA54613.1	X77463	Manihot esculenta	UTP-glucose glucosyltransferase. CGT6.
BAA89008.1	AB027454	Petunia x hybrida	anthocyanidin 3-O-glucosyltransferase. PGT8.
BAA12737.1	D85186	Gentiana triflora	UDP-glucose:flavonoid-3-glucosyltransferase.
SEQ ID NO: 576			
CAB60277.1	AJ002586	Solanum tuberosum	UCP.
CAA72107.1	Y11220	Solanum tuberosum	mitochondrial uncoupling protein.
BAA92172.1	AB024733	Symplocarpus renifolius	SfUCPa. SfUCPa.
BAB40658.1	AB049998	Oryza sativa	uncoupling protein. OsUCP2.
BAA92173.1	AB024734	Symplocarpus renifolius	SfUCPb. SfUCPb.
BAB16385.1	AB042429	Triticum aestivum	uncoupling protein. WhUCP1b.
BAB16384.1	AB042428	Triticum aestivum	uncoupling protein. WhUCP1a.

BAB40657.1	AB049997	Oryza sativa	uncoupling protein. OsUCP1.
SEQ ID NO: 577			
AAA19571.1	U10150	Brassica napus	calcium binding. calmodulin. bcm1.
AAA87347.1	M88307	Brassica juncea	calmodulin.
AAA92681.1	U13882	Pisum sativum	calcium-binding protein. calmodulin.
AAA33706.1	M80836	Petunia x hybrida	calmodulin. CAM81.
CAA43143.1	X60738	Malus x domestica	Calmodulin. CaM.
CAA78301.1	Z12839	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin. putative.
CAA42423.1	X59751	Daucus carota	calmodulin. Ccam-1.
AAG27432.1	AF295637	Elaeis guineensis	calmodulin.
AAG11418.1	AF292108	Prunus avium	calmodulin.
AAA34237.1	L20691	Vigna radiata	calmodulin.
AAC49587.1	U49105	Triticum aestivum	calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	Triticum aestivum	calmodulin TaCaM3-3. calcium-binding protein.
AAC49585.1	U49103	Triticum aestivum	calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum	calmodulin TaCaM3-1. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum	calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	Triticum aestivum	calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	Triticum aestivum	calmodulin TaCaM1-1. calcium-binding.
AAA03580.1	L01431	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-2. putative.

AAB36130.1	S81594	Vigna radiata	auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from Fig. 1; arCaM.
AAA33901.1	L18913	Oryza sativa	calcium binding protein, signal transduction. calmodulin. putative.
CAA78287.1	Z12827	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
AAB46588.1	U83402	Capsicum annuum	calmodulin.
AAA32938.1	M27303	Hordeum vulgare	calmodulin.
BAA88540.1	AP000969	Oryza sativa	ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene. Similar to calmodulin. (AF042840).
AAF65511.1	AF108889	Capsicum annuum	calmodulin.
AAC36059.1	AF042840	Oryza sativa	calmodulin. CaM1.
AAA34238.1	L20507	Vigna radiata	calmodulin.
AAA34014.1	L01432	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAA34013.1	L01430	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-1. putative.
CAA36644.1	X52398	Medicago sativa	calmodulin (AA 1-149).
AAB68399.1	U79736	Helianthus annuus	calmodulin. HaCaM.
AAD10244.1	AF030032	Phaseolus vulgaris	calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
AAA33705.1	M80831	Petunia x hybrida	calmodulin-related protein. CAM53.
AAA16320.1	L14071	Bryonia dioica	calmodulin. Bc329. calcium-binding sites (amino acid #): 1. (21..33); 2. (57..68); 3. (94..106); 4. (130..141).
CAA61980.1	X89890	Bidens pilosa	Calmodulin.
AAA33900.1	L18914	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
CAA78288.1	Z12828	Oryza sativa	calcium binding protein, signal transduction. calmodulin.

CAA74307.1	Y13974	<i>Zea mays</i>	calmodulin.
AAC49583.1	U48692	<i>Triticum aestivum</i>	calmodulin TaCaM2-3. calcium-binding protein.
AAC49582.1	U48691	<i>Triticum aestivum</i>	calmodulin TaCaM2-2. calcium-binding protein.
AAA85157.1	U20297	<i>Solanum tuberosum</i>	calcium-binding protein. calmodulin.
AAA85156.1	U20296	<i>Solanum tuberosum</i>	calcium-binding protein. calmodulin.
AAA62351.1	U20295	<i>Solanum tuberosum</i>	calcium-binding protein. calmodulin.
AAA85155.1	U20294	<i>Solanum tuberosum</i>	calcium-binding protein. calmodulin.
CAA46150.1	X65016	<i>Oryza sativa</i>	calmodulin. cam.
AAD10246.1	AF030034	<i>Phaseolus vulgaris</i>	calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
AAF73157.1	AF150059	<i>Brassica napus</i>	calmodulin. CaM1. involved in seed germination.
CAA54583.1	X77397	<i>Zea mays</i>	calmodulin. CaM2.
SEQ ID NO: 578			
AAF01764.2	AF184277	<i>Glycine max</i>	homeodomain-leucine zipper protein 56. Hdl56. transcription factor.
BAA21017.1	D26578	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.
AAD37697.1	AF145728	<i>Oryza sativa</i>	homeodomain leucine zipper protein. Oshox4. transcription factor.
CAB67118.1	Y17306	<i>Lycopersicon esculentum</i>	homeodomain protein. h52.
AAF01765.1	AF184278	<i>Glycine max</i>	homeodomain-leucine zipper protein 57. Hdl57. transcription factor.
BAA05624.1	D26575	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.
BAA93466.1	AB028078	<i>Physcomitrella patens</i>	homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.
BAA93465.1	AB028077	<i>Physcomitrella patens</i>	homeobox protein PpHB6. PpHB6. homeodomain-leucine zipper gene.



BAA93464.1	AB028076	Physcomitrella patens	homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.
BAA05622.1	D26573	Daucus carota	transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.
BAA05625.1	D26576	Daucus carota	transcriptional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.
BAA05623.1	D26574	Daucus carota	transcriptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.
AAD37698.1	AF145729	Oryza sativa	homeodomain leucine zipper protein. Oshox5. transcription factor.
BAA93461.1	AB028073	Physcomitrella patens	homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.
BAA93467.1	AB028079	Physcomitrella patens	homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.
BAA93468.1	AB028080	Physcomitrella patens	homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.
BAA93460.1	AB028072	Physcomitrella patens	homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.
AAD37699.1	AF145730	Oryza sativa	homeodomain leucine zipper protein. Oshox6. transcription factor.
CAA06717.1	AJ005820	Craterostigma plantagineum	transcription factor. homeodomain leucine zipper protein. hb-1.
BAA93463.1	AB028075	Physcomitrella patens	homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.
CAA65456.2	X96681	Oryza sativa	transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.
AAF19980.1	AF211193	Oryza sativa	homeodomain-leucine zipper transcription factor. Hox1. hox1.
AAK31270.1	AC079890	Oryza sativa	homeodomain leucine zipper protein hox1. OSJNBb0089A17.12.
CAA06728.1	AJ005833	Craterostigma plantagineum	transcription factor. homeodomain leucine zipper protein. hb-2.
AAD37696.1	AF145727	Oryza sativa	homeodomain leucine zipper protein. Oshox3. transcription factor.
SEQ ID NO: 580			
AAD32141.1	AF123503	Nicotiana tabacum	Nt-gh3 deduced protein.
CAA42636.1	X60033	Glycine max	auxin-responsive GH3 product. GH3.

BAA96221.1	AP002094	Oryza sativa	ESTs C19814(E10971),AU090481(E10971) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, sequence from clones T3F17, F11C10, F13A10; auxin-responsive GH3-like protein (AC006526).
SEQ ID NO: 581			
AAD13632.1	AF059488	Lycopersicon esculentum	expansin precursor. Exp4.
AAF32410.1	AF230277	Triphysaria versicolor	alpha-expansin 2.
CAA04385.1	AJ000885	Brassica napus	Cell wall extension in plants. Expansin.
CAB46492.1	AJ243340	Lycopersicon esculentum	expansin9. exp9.
AAC63088.1	U82123	Lycopersicon esculentum	expansin. LeEXP1. fruit ripening regulated expansin.
CAA06271.2	AJ004997	Lycopersicon esculentum	expansin18. exp18.
AAF62182.1	AF247164	Oryza sativa	alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.
AAF35900.1	AF230331	Zinnia elegans	expansin. Exp1.
AAG13982.1	AF297521	Prunus avium	expansin 1. Exp1. PruavExp1.
AAC33529.1	U93167	Prunus armeniaca	expansin. PA-Exp1.
AAF21101.1	AF159563	Fragaria x ananassa	expansin. Exp2. ripening regulated.
AAF35901.1	AF230332	Zinnia elegans	expansin 2.
AAG13983.1	AF297522	Prunus avium	expansin 2. Exp2. PruavExp2.
AAC33530.1	AF038815	Prunus armeniaca	expansin. Exp2.
BAB19676.1	AB029083	Prunus persica	expansin. PchExp1.
AAB40637.1	U64893	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAB37746.1	U30382	Cucumis sativus	expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.

CAC19184.1	AJ291817	Cicer arietinum	expansin.
AAD47901.1	AF085330	Pinus taeda	expansin.
AAB40634.1	U64890	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAF32409.1	AF230276	Triphysaria versicolor	alpha-expansin 3.
AAC39512.1	AF043284	Gossypium hirsutum	expansin. GhEX1. contains N-terminal signal peptide.
AAB40635.1	U64891	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAC96081.1	AF049354	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.
AAB38074.1	U30477	Oryza sativa	induces extension (creep) in plant cell walls. expansin Os-EXP2. Os-EXP2. former gene name RiExB.
AAG32921.1	AF184233	Lycopersicon esculentum	expansin. Exp10.
AAB81662.1	U85246	Oryza sativa	expansin. Os-EXP4.
AAD49956.1	AF167360	Rumex palustris	expansin. EXP1.
AAB40636.1	U64892	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAF32411.1	AF230278	Triphysaria versicolor	alpha-expansin 1.
AAC96080.1	AF049353	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP4. cell wall protein.
AAF35902.1	AF230333	Zinnia elegans	expansin 3.
CAB43197.1	AJ239068	Lycopersicon esculentum	cell wall loosening enzyme. expansin2. exp2.
AAC64201.1	AF096776	Lycopersicon esculentum	expansin. LeEXP2.

AAAF17570.1	AF202119	Marsilea quadrifolia	alpha-expansin. EXP1. Mq-EXP1.
AAD13633.1	AF059489	Lycopersicon esculentum	expansin precursor. Exp5.
AAF62181.1	AF247163	Oryza sativa	alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.
AAAF17571.1	AF202120	Regnellidium diphyllum	alpha-expansin. EXP1. Rd-EXP1.
AAF62180.1	AF247162	Oryza sativa	alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.
CAC19183.1	AJ291816	Cicer arietinum	expansin.
CAC06433.1	AJ276007	Festuca pratensis	expansin. exp2.
BAB32732.1	AB049406	Eustoma grandiflorum	expansin. Eg Expansin.
AAG01875.1	AF291659	Striga asiatica	alpha-expansin 3. Exp3.
AAB37749.1	U30460	Cucumis sativus	expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
AAC96077.1	AF049350	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
AAC96079.1	AF049352	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.
AAG32920.1	AF184232	Lycopersicon esculentum	expansin. Exp8.
CAA69105.1	Y07782	Oryza sativa	expansin. RiExA.
AAC96078.1	AF049351	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
SEQ ID NO: 583			
BAA85412.1	AP000615	Oryza sativa	ESTs AU065232(E60855), C23624(S1554), AU078241(E60855) correspond to a region of the predicted gene.; similar to putative adenylate kinase. (AC005896).
BAA01181.1	D10335	Oryza sativa	adenylate kinase-b. Adk-b.
BAA01180.1	D10334	Oryza sativa	adenylate kinase-a. Adk-a.
BAA94761.1	AB041773	Oryza sativa	adenylate kinase. Adk-a.

AAB68604.1	U82330	Prunus armeniaca	adenylate kinase homolog.
AAF23372.1	AF187063	Oryza sativa	catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase b. ura6.
AAF23371.1	AF187062	Oryza sativa	catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase a. ura6.
AAD41679.1	AF086603	Ceratopteris richardii	adenylate kinase. ADK1.
BAA85443.1	AP000616	Oryza sativa	similar to UMP/CMP kinase (AF000147).
SEQ ID NO: 584			
BAA87052.2	D88273	Hordeum vulgare	nicotianamine aminotransferase A. naat-A.
BAA87055.1	AB024006	Hordeum vulgare	nicotianamine aminotransferase. naat-A.
BAA87053.1	AB005788	Hordeum vulgare	nicotianamine aminotransferase B. naat-b. NAAT-B.
BAA87054.1	AB024006	Hordeum vulgare	nicotianamine aminotransferase. naat-B.
BAA77261.1	AB007405	Oryza sativa	alanine aminotransferase. AlaAT.
BAA77260.1	AB007404	Oryza sativa	alanine aminotransferase. AlaAT.
CAA49199.1	X69421	Panicum miliaceum	alanine aminotransferase. pAlaAT-2.
AAB01685.1	U31975	Chlamydomonas reinhardtii	catalyzes the transfer of -NH <sub>2</sub> from ala to 2-oxoglutarate. alanine aminotransferase. The translation start site has not been experimentally tested, but a 55 kDa product can be detected in Western blot.
AAC62456.1	AF055898	Zea mays	alanine aminotransferase. alt. AlaAT.
CAA81231.1	Z26322	Hordeum vulgare	alanine aminotransferase.
SEQ ID NO: 586			
AAB94589.1	AF022460	Glycine max	CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.
AAA32913.1	M32885	Persea americana	cytochrome P-450LXXIA1 (cyp71A1).
AAA19701.1	L24438	Thlaspi arvense	cytochrome P450.

BAB40324.1	AB037245	<i>Asparagus officinalis</i> cytochrome P450. ASPI-2.
AAC39318.1	AF029858	<i>Sorghum bicolor</i> second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.
BAB40323.1	AB037244	<i>Asparagus officinalis</i> cytochrome P450. ASPI-1.
CAA71517.1	Y10493	<i>Glycine max</i> putative cytochrome P450.
AAB61965.1	U48435	<i>Solanum chacoense</i> putative cytochrome P450.
CAA70575.1	Y09423	<i>Nepeta racemosa</i> cytochrome P450. CYP71A5.
CAA71513.1	Y10489	<i>Glycine max</i> putative cytochrome P450.
AAB61964.1	U48434	<i>Solanum chacoense</i> putative cytochrome P450.
AAD47832.1	AF166332	<i>Nicotiana tabacum</i> cytochrome P450.
AAB94588.1	AF022459	<i>Glycine max</i> CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAF27282.1	AF122821	<i>Capsicum annuum</i> cytochrome P450. PepCYP.
CAA50312.1	X70981	<i>Solanum melongena</i> P450 hydroxylase. CYPEG2.
CAA83941.1	Z33875	<i>Mentha x piperita</i> cytochrome P-450 oxidase.
AAG44132.1	AF218296	<i>Pisum sativum</i> cytochrome P450. P450 isolog.
CAA70576.1	Y09424	<i>Nepeta racemosa</i> cytochrome P450. CYP71A6.
AAD44151.1	AF124816	<i>Mentha x piperita</i> cytochrome p450 isoform PM17.
BAA03635.1	D14990	<i>Solanum melongena</i> Cytochrome P-450EG4.
CAA50645.1	X71654	<i>Solanum melongena</i> P450 hydroxylase.
AAB69644.1	AF000403	<i>Lotus japonicus</i> putative cytochrome P450. LjNP450.
AAD37433.1	AF150881	<i>Lycopersicon esculentum x Lycopersicon peruvianum</i> catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.

CAA65580.1	X96784	Nicotiana tabacum cytochrome P450. hsr515.
AAD44152.1	AF124817	Mentha x piperita cytochrome p450 isoform PM2.
CAA64635.1	X95342	Nicotiana tabacum cytochrome P450. hsr515. hypersensitivity-related gene.
AAG14962.1	AF214008	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H2.
AAG14961.1	AF214007	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H1.
CAB56503.1	AJ238612	Catharanthus roseus cytochrome P450.
AAG14963.1	AF214009	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H3.
AAK38088.1	AF321864	Lolium rigidum putative cytochrome P450.
AAD44150.1	AF124815	Mentha spicata cytochrome p450.
AAK38084.1	AF321860	Lolium rigidum putative cytochrome P450.
AAD56282.1	AF155332	Petunia x hybrida flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAK38087.1	AF321863	Lolium rigidum putative cytochrome P450.
AAK38083.1	AF321859	Lolium rigidum putative cytochrome P450.
AAB94584.1	AF022157	Glycine max capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
CAA71514.1	Y10490	Glycine max putative cytochrome P450.
BAA12159.1	D83968	Glycine max Cytochrome P-450 (CYP93A1).
BAB39252.1	AP002968	Oryza sativa putative cytochrome P450. P0416G11.1.
CAA50155.1	X70824	Solanum melongena flavonoid hydroxylase (P450). CYP75.
SEQ ID NO: 587		
CAA60120.1	X86222	Pisum sativum heat shock protein. hsp22.
AAF37726.1	AF237957	Euphorbia esula LMW heat shock protein. putative 22 kDa mitochondrial heat shock protein.

BAA32547.1	AB017134	Lycopersicon esculentum mitochondrial small heat shock protein. LEMTSHP.
CAA33388.1	X15333	Chenopodium rubrum heat shock protein (AA 1-204).
AAB03096.1	U21722	Glycine max Hsp23.9. Gmhsp23.9. low molecular weight heat shock protein.
AAC12279.1	AF035460	Zea mays low molecular weight heat shock protein precursor. hsp22.
AAD03604.1	AF104107	Triticum aestivum small heat shock protein Hsp23.5. mRNA not present, or only at very low levels, prior to heat stress; mRNA abundant after two hours at 40C.
AAB01557.1	L47741	Picea glauca mitochondria-localized low molecular weight heat shock protein 23.5. EMB22, SMW HSP23.5.
AAD03605.1	AF104108	Triticum aestivum small heat shock protein Hsp23.6.
CAA38037.1	X54103	Plastid Petunia x hybrida heat shock protein. hsp21.
AAF19022.1	AF197942	Funaria hygrometrica chloroplast-localized small heat shock protein 22. CPsHSP22.
AAB49626.1	U59917	Lycopersicon esculentum chromoplast-associated hsp20. pTOM111. small molecular weight heat shock protein.
AAB07023.1	U66300	Chloroplast Lycopersicon esculentum heat shock protein. HSP21.
BAA29064.1	D88584	Nicotiana tabacum heat shock protein 26 (Type I). Nthsp26a. plastid-localized small heat shock protein.
AAF19021.1	AF197941	Funaria hygrometrica chloroplast-localized small heat shock protein. CPsHSP21. CPsHS 21.
BAA78385.1	AB020973	Oryza sativa heat shock protein 26. Oshsp26. chloroplast-localized small heat shock protein.
CAA41219.1	X58280	Triticum aestivum heat shock protein 26.6. Tahsp26.6.
AAC96315.1	AF097657	Triticum aestivum heat shock protein HSP26. hsp26.6. similar to the Triticum aestivum hsp26.6G2 protein encoded by the sequence presented in GenBank Accession Number L41503; 26 kDa protein.
AAC96316.1	AF097658	Triticum aestivum heat shock protein HSP26. hsp26.6. 26 kDa protein.
AAC96314.1	AF097656	Triticum aestivum heat shock protein HSP26. hsp26.6. 26 kDa protein.
CAA47745.1	X67328	Triticum aestivum heat shock protein 26.6B. hsp 26.6B.
AAC96317.1	AF097659	Triticum aestivum heat shock protein HSP26. hsp26.6. 26 kDa protein.



AAA33477.1	L28712	<i>Zea mays</i>	heat shock protein 26. HSP26. plastid-localized low molecular weight hsp.
BAA29066.1	AB006043	<i>Nicotiana sylvestris</i>	heat shock protein 26. hsp26. plastid-localized small heat shock protein.
BAA29067.1	AB006044	<i>Nicotiana tomentosiformis</i>	heat shock protein 26. hsp26. plastid-localized small heat shock protein.
BAA29065.1	AB006041	<i>Nicotiana tabacum</i>	heat shock protein 26 (Type I). Nthsp26a. plastid-localized small heat shock protein 26.
AAC01570.1	AF019144	<i>Agrostis stolonifera</i> var. <i>palustris</i>	low molecular weight heat shock protein.
AAD30452.1	AF123255	<i>Lycopersicon esculentum</i>	17.7 kD class I small heat shock protein. HSP17.7.
CAA39603.1	X56138	<i>Lycopersicon esculentum</i>	small heat shock protein (class I).
AAD30453.1	AF123256	<i>Lycopersicon esculentum</i>	17.8 kD class I small heat shock protein. HSP17.8.
AAD30454.1	AF123257	<i>Lycopersicon esculentum</i>	17.6 kD class I small heat shock protein. HSP17.6.
AAD49336.1	AF166277	<i>Nicotiana tabacum</i>	low molecular weight heat-shock protein. LHS-1. TLHS-1.
AAF34133.1	AF161179	<i>Malus x domestica</i>	low molecular weight heat shock protein. Hsp1.
AAC39360.1	U63631	<i>Fragaria x ananassa</i>	LMW heat shock protein.
AAA61632.1	U08601	<i>Papaver somniferum</i>	low molecular weight heat-shock protein.
CAA08908.1	AJ009880	<i>Castanea sativa</i>	molecular chaperone. cytosolic class I small heat-shock protein HSP17.5. hsp17.5.
AAA33975.1	M11395	<i>Glycine max</i>	small heat shock protein.
CAA63570.1	X92983	<i>Pseudotsuga menziesii</i>	low molecular weight heat-shock protein.
AAB03893.1	M11318	<i>Glycine max</i>	17.5 kd heat shock protein Gmhsp17.6L.
CAA25578.1	X01104	<i>Glycine max</i>	heat shock protein 6871 (aa 1-153).
AAB72109.1	AF022217	<i>Brassica rapa</i>	low molecular weight heat-shock protein. BcHSP17.6. 17.6 kDa; cytosolic class I.
CAA46641.1	X65725	<i>Zea mays</i>	heat shock protein 17.2. Zmhsp 17.2. Class I low molecular weight heat shock protein.
CAB08441.1	Z95153	<i>Helianthus annuus</i>	17.6 kD class I small heat-shock protein HSP17.6. Ha hsp17.6.

AAA33974.1	M11317	Glycine max 17.6 kd heat shock protein Gmhsp17.6L.
SEQ ID NO: 588		
AAA32913.1	M32885	Persea americana cytochrome P-450LXXIA1 (cyp71A1).
AAA19701.1	L24438	Thlaspi arvense cytochrome P450.
AAC39318.1	AF029858	Sorghum bicolor second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p- hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.
BAB40323.1	AB037244	Asparagus officinalis cytochrome P450. ASPI-1.
BAB40324.1	AB037245	Asparagus officinalis cytochrome P450. ASPI-2.
AAB94589.1	AF022460	Glycine max CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
AAB94584.1	AF022157	Glycine max capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
AAB61965.1	U48435	Solanum chacoense putative cytochrome P450.
AAF27282.1	AF122821	Capsicum annuum cytochrome P450. PepCYP.
CAB56503.1	AJ238612	Catharanthus roseus cytochrome P450.
AAD47832.1	AF166332	Nicotiana tabacum cytochrome P450.
AAB94588.1	AF022459	Glycine max CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAB61964.1	U48434	Solanum chacoense putative cytochrome P450.
CAA71517.1	Y10493	Glycine max putative cytochrome P450.
CAA50645.1	X71654	Solanum melongena P450 hydroxylase.
BAA03635.1	D14990	Solanum melongena Cytochrome P-450EG4.

CAA50312.1	X70981	Solanum melongena	P450 hydroxylase. CYPEG2.
CAA71514.1	Y10490	Glycine max	putative cytochrome P450.
AAB69644.1	AF000403	Lotus japonicus	putative cytochrome P450. LjNP450.
CAA70576.1	Y09424	Nepeta racemosa	cytochrome P450. CYP71A6.
AAD44151.1	AF124816	Mentha x piperita	cytochrome p450 isoform PM17.
AAK38084.1	AF321860	Lolium rigidum	putative cytochrome P450.
CAA83941.1	Z33875	Mentha x piperita	cytochrome P-450 oxidase.
AAK38083.1	AF321859	Lolium rigidum	putative cytochrome P450.
AAD44152.1	AF124817	Mentha x piperita	cytochrome p450 isoform PM2.
BAB39252.1	AP002968	Oryza sativa	putative cytochrome P450. P0416G11.1.
AAD44150.1	AF124815	Mentha spicata	cytochrome p450.
AAK38087.1	AF321863	Lolium rigidum	putative cytochrome P450.
AAK38082.1	AF321858	Lolium rigidum	putative cytochrome P450.
CAA57423.1	X81829	Zea mays	cytochrome P450. CYP71C2. family CYP71, subfamily CYP71C.
CAA72208.1	Y11404	Zea mays	cytochrome p450. cyp71c2.
CAC27827.1	AJ295719	Catharanthus roseus	geraniol hydroxylase. cytochrome P450. cyp71.
AAG44132.1	AF218296	Pisum sativum	cytochrome P450. P450 isolog.
AAK38088.1	AF321864	Lolium rigidum	putative cytochrome P450.
AAG14963.1	AF214009	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H3.
CAA57424.2	X81830	Zea mays	cytochrome P450. CYP71C3. family CYP71, subfamily CYP71C.
CAA72207.1	Y11403	Zea mays	cytochrome p450. cyp71c3.

AAG14962.1 AF214008 Brassica napus  
cytochrome p450-dependent monooxygenase. BNF5H2.

AAG14961.1 AF214007 Brassica napus  
cytochrome p450-dependent monooxygenase. BNF5H1.

BAA12159.1 D83968 Glycine max  
Cytochrome P-450 (CYP93A1).

BAB40322.1 AB036772 Triticum aestivum  
cytochrome P450. N-1.

SEQ ID NO: 593

BAA09645.1 D63331 Nicotiana tabacum  
Indole-3-acetonitrile hydrolysis. nitrilase. TNIT4. Indole-3-acetonitrile hydrolysis, indole-3-acetic acid biosynthesis.

BAA11770.1 D83078 Nicotiana tabacum  
indole-3-acetonitrile hydrolysis. nitrilase. TNIT4B. indole-3-acetonitrile hydrolysis, indole-3-acetic acid biosynthesis.

BAA77679.1 AB027054 Oryza sativa  
nitrilase-like protein. ONIT4.

SEQ ID NO: 595

AAG01147.1 AF283816 Pinus taeda  
calreticulin. calcium-binding protein.

CAA05161.1 AJ002057 Beta vulgaris  
calreticulin.

AAB71419.1 U74630 Ricinus communis  
calreticulin.

AAB71420.1 U74631 Ricinus communis  
endoplasmic reticulum calcium binding protein. calreticulin.

CAA95999.1 Z71395 Nicotiana plumbaginifolia  
ER Ca<sup>2+</sup> binding protein. calreticulin. cal1.

AAD17490.1 AF052040 Berberis stolonifera  
possible molecular chaperon. calreticulin. calcium binding protein of the endoplasmic reticulum.

AAD32207.1 AF134733 Prunus armeniaca  
calcium-binding protein calreticulin.

CAA61939.1 X89813 Zea mays  
Calreticulin precursor.

AAA32948.1 L27348 Hordeum vulgare  
calcium binding protein. calreticulin. CRH1.

AAA32949.1 L27349 Hordeum vulgare  
calcium binding protein. calreticulin. CRH2.

AAF01470.1 AF190454 Zea mays  
calreticulin. CRT. calcium binding protein.

CAB54526.1 AJ000765 Chlamydomonas reinhardtii  
calreticulin.

AAB70919.1	AF019376	Brassica napus calreticulin. Crt1. calcium binding protein; similar to A. thaliana calreticulin encoded by GenBank Accession Number U66343.
BAA85118.1	AB018243	Solanum melongena calreticulin-like protein. EEF22.
CAA54975.1	X78057	Zea mays calreticulin. CRH.
CAA57914.1	X82578	Parthenium argentatum calreticulin. 111R.
AAK15502.1	AF325720	Pennisetum ciliare calreticulin-like protein. Pcp4.
BAA77025.1	AB026251	Lithospermum erythrorhizon calreticulin.
SEQ ID NO: 596		
BAA12206.1	D84061	Spinacia oleracea phosphoserine aminotransferase.
SEQ ID NO: 597		
AAF73124.1	AF148534	Lycopersicon esculentum whitefly-induced gp91-phox. Wf1. mammalian gp91-phox homolog; respiratory burst oxidase homolog; putative NADPH oxidase; similar to neutrophil NADPH oxidase gp91- phox subunit; similar to Arabidopsis thaliana Rboh and Oryza sativa Rboh; similar to Caenorhabditis elegans PhoX-like proteins.
AAF73104.1	AF147783	Lycopersicon esculentum whitefly-induced gp91-phox. Wf1. mammalian gp91-phox homolog; respiratory burst oxidase homolog; putative NADPH oxidase; similar to neutrophil NADPH oxidase gp1-phox subunit; similar to Arabidopsis thaliana Rboh and Oryza sativa Rboh.
AAD25300.1	AF088276	Lycopersicon esculentum NADPH oxidase. RBOH1. gp91; phox homolog.
AAB87790.1	AF015302	Oryza sativa RbohAosp. putative NADPH oxidase; intrinsic plasma membrane protein; similar to the neutrophil NADPH oxidase gp91phox subunit; contains RanGAP1 domain; similar to O. sativa NAD(P)H oxidase sequence with GenBank Accession Number X93301.
CAA63704.1	X93301	Oryza sativa NAD(P)H oxidase. rbohA.
AAD24966.1	AF109150	Lycopersicon esculentum NADPH oxidase. gp91; phox homolog.
AAD25225.1	AF088279	Potamogeton crispus NADPH oxidase. RBOH1. gp91; phox homolog.
SEQ ID NO: 599		
CAC21424.1	AJ278332	Lycopersicon esculentum involved in octadecanoid biosynthesis. 12-oxophytodienoate reductase 3. opr3.
BAB40340.1	AB044940	Pisum sativum 12-oxophytodienoic acid 10, 11-reductase. OPDAR.

CAB43506.1	AJ242551	Lycopersicon esculentum	involved in jasmonic acid biosynthesis. 12-oxophytodienoate reductase. opr.
CAC21423.1	AJ278331	Lycopersicon esculentum	involved in octadecanoid biosynthesis. putative 12-oxophytodienoate reductase 2. opr2.
CAB97122.1	AJ297421	Daucus carota	oxidoreductase. putative 12-oxophytodienoate reductase. opr2.
SEQ ID NO: 602			
AAB37246.1	U58971	Nicotiana tabacum	calmodulin-binding protein. TCB60.
SEQ ID NO: 603			
AAK15006.1	AF233433	Brassica napus	arginase. similar to Arabidopsis thaliana and Glycine max arginase.
AAK07744.1	AF130440	Pinus taeda	converts L-arginine to L-ornithine and urea. arginase. ARS20. L-arginine amidinohydrolase.
AAC04613.1	AF035671	Glycine max	hydrolysis of L-Arg to L-Orn and urea. arginase. pAG1. L-Arg amidinohydrolase.
SEQ ID NO: 605			
CAA81210.1	Z26251	Helianthus tuberosus	Catalyzes the reduction of cytochrome P450 in microsomes. NADPH-ferrihemoprotein reductase.
AAB02721.1	U58629	Helianthus tuberosus	NADPH-ferrihemoprotein oxidoreductase. HTR2. NADPH-cytochrome P450 reductase isoform.
CAC27143.1	AJ132538	Picea abies	NADPH-cytochrome P450 reductase.
AAA79131.1	U10545	Chlamydomonas reinhardtii	ferredoxin-NADP+ reductase. fnr.
CAA55406.1	X78851	Chlamydomonas reinhardtii	ferredoxin NADP reductase.
AAB40978.1	U22328	Volvox carteri	ferredoxin-NADP+ reductase. fnr. FNR.
AAA33029.1	M25528	Mesembryanthemum crystallinum	ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1).
CAA30978.1	X12446	Pisum sativum	ferredoxin-NADH+ reductase preprotein (AA -52 to 308).
BAA13417.1	D87547	Oryza sativa	precursor ferredoxin-NADP+ oxidoreductase.
AAA21758.1	U14956	Vicia faba	photosynthetic electron transport. ferredoxin NADP+ reductase precursor. fnr.
AAA34029.1	M86349	Spinacia oleracea	ferredoxin-NADP oxidoreductase. precursor protein.
CAB71293.1	AJ250378	Capsicum annuum	chloroplast ferredoxin-NADP+ oxidoreductase precursor. fnr.

CAA74359.1	Y14032	Nicotiana tabacum	ferredoxin--NADP(+) reductase. fnr.
BAA88236.1	AB035644	Zea mays	NADP+ oxidoreductase. ferredoxin. L-FNRI.
BAA88237.1	AB035645	Zea mays	NADP+ oxidoreductase. ferredoxin. L-FNRII.
BAA20365.1	AB004307	Nicotiana tabacum	ferredoxin-NADP oxidoreductase.
BAA07479.1	D38445	Oryza sativa	root ferredoxin-NADP+ reductase. root FNR. nitrate assimilation pathway.
BAA02248.1	D12815	Oryza sativa	ferredoxin-NADP+ reductase enzyme.
BAA04232.1	D17410	Oryza sativa	ferredoxin-NADP+ reductase.
BAA90642.1	AP001129	Oryza sativa	ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; Similar to Oryza sativa, ferredoxin-NADP+ reductase. (D17790).
BAA85425.1	AP000616	Oryza sativa	ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790).
BAA04616.1	D17790	Oryza sativa	ferredoxin-NADP+ reductase.
AAB40034.1	U10418	Zea mays	ferredoxin-NADP reductase precursor.
CAA67796.1	X99419	Pisum sativum	ferredoxin NADP oxidoreductase.
AAK09367.1	AF321525	Pisum sativum	ferredoxin-NADP+ reductase. FNR.
AAK09370.1	AF321528	Pisum sativum	ferredoxin-NADP+ reductase. FNR.
AAK09369.1	AF321527	Pisum sativum	ferredoxin-NADP+ reductase. FNR.
AAK09368.1	AF321526	Pisum sativum	ferredoxin-NADP+ reductase. FNR.
SEQ ID NO: 606			
BAA82107.1	AB022693	Nicotiana tabacum	transcription factor. NtWRKY1.
AAC31956.1	AF080595	Pimpinella brachycarpa	zinc finger protein. ZFP1. WRKY1.
AAC49527.1	U48831	Petroselinum crispum	WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.

AAD55974.1	AF121353	Petroselinum crispum	zinc-finger type transcription factor WRKY1. WRKY1.
BAA77383.1	AB020590	Nicotiana tabacum	transcription factor NtWRKY2.
AAD32677.1	AF140554	Avena sativa	DNA-binding protein WRKY1. wrky1. putative transcription factor.
CAA88326.1	Z48429	Avena fatua	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
BAA86031.1	AB026890	Nicotiana tabacum	transcription factor NtWRKY4.
AAD16139.1	AF096299	Nicotiana tabacum	DNA-binding protein 2. WRKY2. transcription factor.
AAC37515.1	L44134	Cucumis sativus	SPF1-like DNA-binding protein.
AAF23898.1	AF193802	Oryza sativa	zinc finger transcription factor WRKY1.
AAK16171.1	AC079887	Oryza sativa	putative DNA-binding protein. OSJNBa0040E01.10.
AAC49529.1	U58540	Petroselinum crispum	WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
AAD16138.1	AF096298	Nicotiana tabacum	DNA-binding protein 1. WRKY1. transcription factor.
BAB19096.1	AP002839	Oryza sativa	putative DNA-binding protein homolog. P0688A04.2.
BAB19075.1	AP002744	Oryza sativa	putative DNA-binding protein homolog. P0006C01.17.
AAK16170.1	AC079887	Oryza sativa	putative DNA binding protein. OSJNBa0040E01.4.
CAB97004.1	AJ278507	Solanum tuberosum	putative transcription factor. WRKY DNA binding protein. WRKY1.
BAB18313.1	AP002865	Oryza sativa	putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
AAD38283.1	AC007789	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAB40073.1	AP003074	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
AAC49528.1	U56834	Petroselinum crispum	DNA-binding. WRKY3. WRKY-type DNA-binding protein.
BAB16432.1	AB041520	Nicotiana tabacum	WRKY transcription factor Nt-SubD48. Nt-SubD48.
BAA77358.1	AB020023	Nicotiana tabacum	WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.



AAD32676.1	AF140553	<i>Avena sativa</i>	DNA-binding protein WRKY3. wrky3. putative transcription factor.
CAA88331.1	Z48431	<i>Avena fatua</i>	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAG35658.1	AF204925	<i>Petroselinum crispum</i>	transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.
AAG46150.1	AC018727	<i>Oryza sativa</i>	putative DNA-binding protein. OSJNBa0056G17.18.
AAD27591.1	AF121354	<i>Petroselinum crispum</i>	binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.
AAG35659.1	AF204926	<i>Petroselinum crispum</i>	transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.
CAB66338.1	AJ279697	<i>Betula pendula</i>	wrky-type DNA binding protein. wrky.
AAF61864.1	AF193771	<i>Nicotiana tabacum</i>	DNA-binding protein 4. WRKY4. transcription factor.
AAF61863.1	AF193770	<i>Nicotiana tabacum</i>	DNA-binding protein 3. WRKY3. transcription factor.
SEQ ID NO: 608			
BAA87853.1	AP000816	<i>Oryza sativa</i>	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
AAK21965.1	AY028699	<i>Brassica napus</i>	receptor protein kinase PERK1.
BAB21240.1	AP002953	<i>Oryza sativa</i>	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAB19337.1	AP003044	<i>Oryza sativa</i>	putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
BAA92836.1	AB032473	<i>Brassica oleracea</i>	S18 S-locus receptor kinase. SRK18.
AAB61708.1	U93048	<i>Daucus carota</i>	somatic embryogenesis receptor-like kinase. SERK.
BAA23676.1	AB000970	<i>Brassica rapa</i>	receptor kinase 1. BcRK1.
AAK00425.1	AC069324	<i>Oryza sativa</i>	Putative protein kinase. OSJNBa0071K19.11.
BAB39873.1	AP002882	<i>Oryza sativa</i>	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAD21872.1	AF078082	<i>Phaseolus vulgaris</i>	receptor-like protein kinase homolog RK20-1.

CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
AAF76314.1	AF220603	Lycopersicon esculentum	Fen kinase. Lescfen.
AAK11568.1	AF318492	Lycopersicon hirsutum	Pto-like protein kinase B. LhirPtoB.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
AAB47424.1	U59317	Lycopersicon pimpinellifolium	serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.
AAB47422.1	U59318	Lycopersicon esculentum	serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.

AAC48932.1	U13923	Lycopersicon pimpinellifolium	Fen. putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.
AAF76307.1	AF220602	Lycopersicon pimpinellifolium	Fen kinase.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
SEQ ID NO: 610			
BAB17348.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.32.
BAB17345.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.29.
BAB17126.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.16.
BAB39451.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.24.
BAB17342.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.26.
AAC27489.1	AF077130	Oryza sativa	receptor-like protein kinase.
AAF78018.1	AF238474	Oryza sativa	receptor-like kinase. RLG16. protein kinase.
AAC02535.1	AF044260	Oryza sativa	receptor serine/threonine kinase. protein kinase.
BAB39435.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.2.
AAD46917.1	AF164021	Oryza sativa	receptor kinase.

BAB39438.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.7.
BAB17339.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.23.
AAC49629.1	U51330	Triticum aestivum	rust resistance kinase Lr10. LRK10.
BAB17321.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.1.
BAB17129.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.20.
AAF68398.1	AF237568	Oryza sativa	receptor-like protein kinase. RLG2.
BAB17331.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.12.
BAB17139.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.31.
AAC01746.1	AF044489	Oryza sativa	receptor-like protein kinase. drpk1.
AAF78016.1	AF238472	Oryza sativa	receptor-like kinase. RLG15. protein kinase.
BAB39441.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.11.
BAB17116.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.3.
AAF78044.1	AF248493	Oryza sativa	receptor-like kinase. RLG18. protein kinase.
AAD44029.1	AF085164	Hordeum vulgare	receptor-like kinase LRK10.
BAB17332.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.13. contains ESTs D47575(S13157),AU032665(S13157).
BAB17347.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.31. contains ESTs D47575(S13157),AU032665(S13157).
BAB17344.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.28. contains ESTs D47575(S13157),AU032665(S13157).
BAB17337.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.21. contains ESTs D47575(S13157),AU032665(S13157).
BAB17335.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.17. contains ESTs D47575(S13157),AU032665(S13157).
BAB17115.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.2.
BAB39440.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.10.

BAB39437.1	AP003338	Oryza sativa	receptor-like kinase. OJ1212_B09.6.
AAF78019.1	AF238475	Oryza sativa	receptor-like kinase. RLG17. protein kinase.
BAB17127.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.17.
AAD46916.1	AF164020	Oryza sativa	receptor kinase.
AAF78021.1	AF238477	Oryza sativa	receptor-like kinase. RLG5. protein kinase.
AAD46417.1	AF100767	Oryza sativa	receptor-like kinase. 8ARK3. similar to wheat ARK1AS.
AAD46415.1	AF100765	Oryza sativa	receptor-like kinase. 8ARK1. similar to wheat ARK1AS.
BAB17128.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.18.
AAF68400.1	AF237570	Oryza sativa	receptor-like protein kinase. RLG3.
BAB17323.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.3.
BAB17131.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.22.
AAF68397.1	AF237567	Oryza sativa	receptor-like protein kinase. RLG1.
AAF78015.1	AF238471	Oryza sativa	receptor-like kinase. RLG10. protein kinase.
AAD43962.1	U78762	Triticum aestivum	receptor-like kinase ARK1AS. ARK1AS.
SEQ ID NO: 611			
BAA78764.1	AB023482	Oryza sativa	ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.

BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
CAB51834.1	00069	Oryza sativa	l1332.5. contains eukaryotic protein kinase domain PF.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461), C22360(C11461).
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808), AU056702(S20808).
AAK11567.1	AF318491	Lycopersicon hirsutum	Pto-like protein kinase F. LhirPtoF.
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAC48932.1	U13923	Lycopersicon pimpinellifolium	Fen. putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.
AAB47424.1	U59317	Lycopersicon pimpinellifolium	serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.
AAF76307.1	AF220602	Lycopersicon pimpinellifolium	Fen kinase.
AAK11566.1	AF318490	Lycopersicon hirsutum	Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
AAF76314.1	AF220603	Lycopersicon esculentum	Fen kinase. Lescfen.

AAB47421.1	U59316	<i>Lycopersicon esculentum</i> serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
AAF76313.1	AF220603	<i>Lycopersicon esculentum</i> Pto kinase. LescPth5.
AAB47422.1	U59318	<i>Lycopersicon esculentum</i> serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.
AAG59657.1	AC084319	<i>Oryza sativa</i> putative protein kinase. OSJNBa0004B24.20.
AAF76306.1	AF220602	<i>Lycopersicon pimpinellifolium</i> Pto kinase.
AAB47423.1	U59315	<i>Lycopersicon pimpinellifolium</i> serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
AAC48914.1	U02271	<i>Lycopersicon pimpinellifolium</i> protein kinase.
AAK11568.1	AF318492	<i>Lycopersicon hirsutum</i> Pto-like protein kinase B. LhirPtoB.
BAB21241.1	AP002953	<i>Oryza sativa</i> Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721),D48017(S13927).
AAC27894.1	AF023164	<i>Zea mays</i> leucine-rich repeat transmembrane protein kinase 1. ltk1.
AAF91337.1	AF249318	<i>Glycine max</i> Pti1 kinase-like protein. Pti1b. protein kinase.
AAC61805.1	U28007	<i>Lycopersicon esculentum</i> serine/threonine protein kinase. Pto kinase interactor 1. Pti1. Pti1 kinase.
CAA97692.1	Z73295	<i>Catharanthus roseus</i> receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
AAF91336.1	AF249317	<i>Glycine max</i> Pti1 kinase-like protein. Pti1a. protein kinase.
AAF66615.1	AF142596	<i>Nicotiana tabacum</i> LRR receptor-like protein kinase.
AAB61708.1	U93048	<i>Daucus carota</i> somatic embryogenesis receptor-like kinase. SERK.
AAK11569.1	AF318493	<i>Lycopersicon hirsutum</i> Pto-like protein kinase D. LhirPtoD.
BAA92221.1	AP001278	<i>Oryza sativa</i> Similar to <i>Arabidopsis thaliana</i> chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	<i>Oryza sativa</i> Similar to putative Ser/Thr protein kinase. (AC004218).

AAC27895.1 AF023165 *Zea mays*  
leucine-rich repeat transmembrane protein kinase 2. ltk2.

SEQ ID NO: 612

CAA54613.1 X77463 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT6.

CAA54609.1 X77459 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT1.

CAA54611.1 X77461 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT2.

CAA54612.1 X77462 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT5.

BAB17182.1 AP002843 *Oryza sativa*  
putative UTP-glucose glucosyltransferase. P0407B12.19.

BAB17176.1 AP002843 *Oryza sativa*  
putative UTP-glucose glucosyltransferase. P0407B12.13.

CAB56231.1 Y18871 *Dortheanthus bellidiformis*  
betanidin-5-O-glucosyltransferase.

BAA83484.1 AB031274 *Scutellaria baicalensis*  
UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

AAB36653.1 U32644 *Nicotiana tabacum*  
immediate-early salicylate-induced glucosyltransferase. IS5a.

AAK28303.1 AF346431 *Nicotiana tabacum*  
phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.

CAA59450.1 X85138 *Lycopersicon esculentum*  
twil. homologous to glucosyltransferases.

AAB36652.1 U32643 *Nicotiana tabacum*  
immediate-early salicylate-induced glucosyltransferase. IS10a.

AAK28304.1 AF346432 *Nicotiana tabacum*  
phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.

BAA89009.1 AB027455 *Petunia x hybrida*  
anthocyanin 5-O-glucosyltransferase. PH1.

AAG25643.1 AF303396 *Phaseolus vulgaris*  
UDP-glucosyltransferase HRA25. putative; defense associated.

AAF61647.1 AF190634 *Nicotiana tabacum*  
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAA93039.1 AB033758 *Citrus unshiu*  
limonoid UDP-glucosyltransferase. LGTase.

AAB48444.1 U82367 *Solanum tuberosum*  
UDP-glucose glucosyltransferase.

AAD21086.1 AF127218 *Forsythia x intermedia*  
adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.



AAK16175.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.15.
CAC09351.1	AL442007	Oryza sativa	putative glucosyltransferase. H0212B02.7.
AAD04166.1	AF101972	Phaseolus lunatus	catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
AAF17077.1	AF199453	Sorghum bicolor	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
BAA12737.1	D85186	Gentiana triflora	UDP-glucose:flavonoid-3-glucosyltransferase.
BAB07962.1	AP002524	Oryza sativa	putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
BAA36421.1	AB013596	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.
CAA54610.1	X77460	Manihot esculenta	UTP-glucose glucosyltransferase. CGT4.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
BAA36423.1	AB013598	Verbena x hybrida	UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
CAA30760.1	X07937	Zea mays	UDPglucose flavonoid glycosyl transferase. Bz-W22.
CAA30761.1	X07940	Zea mays	UDPglucose flavonoid glycosyl-transferase. Bz-McC.
CAA31855.1	X13500	Zea mays	UDPglucose:flavonol 3-O-glucosyltransferase.
BAA19659.1	AB002818	Perilla frutescens	flavonoid 3-O-glucosyltransferase. UDP glucose.
BAA89008.1	AB027454	Petunia x hybrida	anthocyanidin 3-O-glucosyltransferase. PGT8.
AAK16172.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.14.
SEQ ID NO: 613			
CAA54609.1	X77459	Manihot esculenta	UTP-glucose glucosyltransferase. CGT1.
CAA54613.1	X77463	Manihot esculenta	UTP-glucose glucosyltransferase. CGT6.

CAA54611.1	X77461	Manihot esculenta	UTP-glucose glucosyltransferase. CGT2.
CAA54612.1	X77462	Manihot esculenta	UTP-glucose glucosyltransferase. CGT5.
BAB17182.1	AP002843	Oryza sativa	putative UTP-glucose glucosyltransferase. P0407B12.19.
BAB17176.1	AP002843	Oryza sativa	putative UTP-glucose glucosyltransferase. P0407B12.13.
CAB56231.1	Y18871	Dorotheanthus bellidiformis	betanidin-5-O-glucosyltransferase.
AAB36653.1	U32644	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS5a.
AAK28303.1	AF346431	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
AAB36652.1	U32643	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
CAA59450.1	X85138	Lycopersicon esculentum	twil. homologous to glucosyltransferases.
BAA83484.1	AB031274	Scutellaria baicalensis	UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAF61647.1	AF190634	Nicotiana tabacum	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAA93039.1	AB033758	Citrus unshiu	limonoid UDP-glucosyltransferase. LGTase.
AAB48444.1	U82367	Solanum tuberosum	UDP-glucose glucosyltransferase.
BAA89009.1	AB027455	Petunia x hybrida	anthocyanin 5-O-glucosyltransferase. PH1.
BAA36421.1	AB013596	Perilla frutescens	UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.
CAC09351.1	AL442007	Oryza sativa	putative glucosyltransferase. H0212B02.7.
BAA12737.1	D85186	Gentiana triflora	UDP-glucose:flavonoid-3-glucosyltransferase.
AAG25643.1	AF303396	Phaseolus vulgaris	UDP-glucosyltransferase HRA25. putative; defense associated.
AAD04166.1	AF101972	Phaseolus lunatus	catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.

CAA54610.1	X77460	Manihot esculenta	UTP-glucose glucosyltransferase. CGT4.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
AAK16172.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.14.
BAA36423.1	AB013598	Verbena x hybrida	UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
AAD21086.1	AF127218	Forsythia x intermedia	adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
AAF17077.1	AF199453	Sorghum bicolor	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
AAK16175.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.15.
BAB07962.1	AP002524	Oryza sativa	putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
CAA31855.1	X13500	Zea mays	UDPglucose:flavonol 3-O-glucosyltransferase.
BAA36422.1	AB013597	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.
BAA89008.1	AB027454	Petunia x hybrida	anthocyanidin 3-O-glucosyltransferase. PGT8.
SEQ ID NO: 614			
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.

BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrk1.
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).

BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAA94529.2	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAA94518.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
BAB07904.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.12.
SEQ ID NO: 619			
CAA72092.1	Y11209	Nicotiana tabacum	protein disulfide-isomerase precursor. PDI.
AAG13988.1	AF298829	Prunus avium	putative protein disulfide-isomerase. PDI.
AAD02069.1	AF036939	Chlamydomonas reinhardtii	redox-regulator of 5'UTR psbA mRNA binding complex and translation. protein disulfide isomerase. localized to ER and chloroplast.
AAC49896.1	AF027727	Chlamydomonas reinhardtii	involved in the redox-regulated binding of chloroplast poly(A)-binding protein to the 5'-UTR of psbA mRNA; regulates chloroplast translational activation. protein disulfide isomerase RB60. PDI.
AAD55566.1	AF110784	Volvox carteri f. nagariensis	protein disulfide isomerase precursor. pdi.
AAB08519.1	L39014	Zea mays	protein disulfide isomerase. pdi. putative.

AAA70344.1	L33250	Hordeum vulgare	catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.
AAA70345.1	L33251	Hordeum vulgare	catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.
CAC21230.1	AJ277379	Triticum turgidum subsp. durum	catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.
AAA19660.1	U11496	Triticum aestivum	protein disulfide isomerase. PDI.
CAC21231.1	AJ277380	Triticum turgidum subsp. durum	catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.
CAC21229.1	AJ277378	Triticum turgidum subsp. durum	catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.
CAC21228.1	AJ277377	Triticum turgidum subsp. durum	catalyzes the formation of disulfide bonds. protein disulfide isomerase. Pdi.
AAB05641.1	U41385	Ricinus communis	protein disulphide isomerase PDI. molecular chaperone.
CAA77575.1	Z11499	Medicago sativa	protein disulfide isomerase.
AAD28260.1	AF131223	Datisca glomerata	protein disulfide isomerase homolog. PDI.
AAA70346.1	L33252	Hordeum vulgare	catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.
BAA92322.1	AB039278	Oryza sativa	protein disulfide isomerase. Pdi.
BAA77026.1	AB026252	Lithospermum erythrorhizon	disulfide-isomerase precursor.
AAC79709.1	AF093614	Acetabularia acetabulum	putative protein disulfide isomerase.
SEQ ID NO: 620			
CAA64413.1	X94943	Lycopersicon esculentum	peroxidase. cevil6.
AAA32676.1	M37637	Arachis hypogaea	cationic peroxidase. PNC2.
BAA82307.1	AB027753	Nicotiana tabacum	peroxidase.
AAB67737.1	L77080	Stylosanthes humilis	cationic peroxidase.
AAD37429.2	AF149279	Phaseolus vulgaris	peroxidase 4 precursor. FBP4. secretory peroxidase.
CAA71494.1	Y10468	Spinacia oleracea	peroxidase. prxr7.

AAD37375.1	AF145349	Glycine max	peroxidase. Prx3.
AAF63024.1	AF244921	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx12 precursor. type III peroxidase.
CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa	signal for ER. peroxidase.
BAB39274.1	AP002971	Oryza sativa	putative peroxidase. P0537A05.2.
AAA65637.1	L13654	Lycopersicon esculentum	peroxidase. TPX1.
CAA40796.1	X57564	Armoracia rusticana	peroxidase. peroxidase precursor.
AAD11482.1	U51192	Glycine max	peroxidase precursor. sEPa2.
CAA80502.1	Z22920	Spirodela polyrrhiza	peroxidase.
BAA77387.1	AB024437	Scutellaria baicalensis	peroxidase 1.
CAA59485.1	X85228	Triticum aestivum	peroxidase. POX2.
BAA07663.1	D42064	Nicotiana tabacum	cationic peroxidase isozyme 38K precursor.
BAA11853.1	D83225	Populus nigra	peroxidase.
BAA07664.1	D42065	Nicotiana tabacum	cationic peroxidase isozyme 40K precursor.
AAD37430.1	AF149280	Phaseolus vulgaris	peroxidase 5 precursor. FBP5. secretory peroxidase.
AAD11481.1	U51191	Glycine max	peroxidase precursor. sEPa1.
CAB94692.1	AJ242742	Ipomoea batatas	Removal of H <sub>2</sub> O <sub>2</sub> , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
BAA03644.1	D14997	Oryza sativa	peroxidase.
AAD43561.1	AF155124	Gossypium hirsutum	bacterial-induced peroxidase precursor. Perx_Goshiko.
BAA06334.1	D30652	Populus kitakamiensis	peroxidase.
BAA92500.1	AP001383	Oryza sativa	ESTs D39300(R3292),AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).

BAA90365.1	AP001081	Oryza sativa	ESTs D24550(R2151),D24265(R1609),AU031848(R2151) correspond to a region of the predicted gene. Similar to cationic peroxidase isozyme 40K precursor (D42065).
BAA89584.1	AP001073	Oryza sativa	ESTs D24550(R2151),D24265(R1609),AU031848(R2151) correspond to a region of the predicted gene. Similar to cationic peroxidase isozyme 40K precursor (D42065).
AAF34416.1	AF172282	Oryza sativa	putative peroxidase. DUPR11.5.
AAC49820.1	AF014469	Oryza sativa	peroxidase. POX5.1. wound inducible.
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa	signal for ER. peroxidase.
BAB39281.1	AP002971	Oryza sativa	putative peroxidase. P0537A05.10. contains ESTs D24657(R2329),AU082066(R2329).
BAA14144.1	D90116	Armoracia rusticana	peroxidase isozyme.
AAB97734.1	AF014502	Glycine max	seed coat peroxidase precursor. Ep. H2O2 oxidoreductase; class III plant peroxidase.
CAA37713.1	X53675	Triticum aestivum	peroxidase.
AAC05277.1	AF049881	Linum usitatissimum	peroxidase FLXPER4. PER4.
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa	signal for ER. peroxidase.
BAA06335.1	D30653	Populus kitakamiensis	peroxidase.
CAA39486.1	X56011	Triticum aestivum	peroxidase.
BAA03911.1	D16442	Oryza sativa	peroxidase.
BAA94962.1	AB042103	Asparagus officinalis	peroxidase. AspPOX1.
AAC49821.1	AF014470	Oryza sativa	peroxidase. POXgX9. expressed in roots.
AAD37427.1	AF149277	Phaseolus vulgaris	peroxidase 1 precursor. FBP1. secretory peroxidase.
CAA76374.2	Y16776	Spinacia oleracea	peroxidase. prx10.
BAA08499.1	D49551	Oryza sativa	peroxidase. poxN.
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa	signal for ER. peroxidase.



AAA34108.1	J02979	Nicotiana tabacum	lignin-forming peroxidase precursor (EC 1.11.1.7).
CAA62226.1	X90693	Medicago sativa	peroxidase1B. prx1B.
CAA59487.1	X85230	Triticum aestivum	peroxidase. pox4.
SEQ ID NO: 626			
CAA98160.1	Z73932	Lotus japonicus	GTP-binding protein. RAB1C. rab1C.
BAA76422.1	AB024994	Cicer arietinum	rab-type small GTP-binding protein.
BAA02116.1	D12548	Pisum sativum	GTP-binding protein.
CAA69701.1	Y08425	Nicotiana plumbaginifolia	small GTP-binding protein. Rab1 subfamily.
AAA80678.1	U38464	Lycopersicon esculentum	small GTP-binding protein. LeRab1A. ; YPT1/Rab1A homolog LeRab1A.
BAA02118.1	D12550	Pisum sativum	GTP-binding protein.
AAB97115.1	U58854	Glycine max	small GTP-binding protein. sra2.
CAA51011.1	X72212	Nicotiana tabacum	ras-related GTP-binding protein. ypt2 homologue.
AAF65510.1	AF108883	Capsicum annuum	small GTP-binding protein.
AAA80680.1	U38466	Lycopersicon esculentum	small GTP-binding protein. LeRab1C. ; YPT1/Rab1A homolog LeRab1C.
CAA98161.1	Z73933	Lotus japonicus	GTP-binding protein. RAB1D. rab1D.
BAA02117.1	D12549	Pisum sativum	GTP-binding protein.
CAA98162.1	Z73934	Lotus japonicus	GTP-binding protein. RAB1E. rab1E.
AAA50159.1	L27417	Glycine max	GTP binding protein.
AAB28535.1	S66160	Oryza sativa	ric1. ras-related GTP binding protein possessing GTPase activity; This sequence comes from Fig. 1.
CAA98159.1	Z73931	Lotus japonicus	GTP-binding protein. RAB1B. rab1B.
BAA02115.1	D12547	Pisum sativum	GTP-binding protein.

CAA66447.1	X97853	Lotus japonicus	GTP-binding protein. RAB1A. rab1A.
AAD10389.1	U35026	Petunia x hybrida	Rab1-like small GTP-binding protein.
AAA80679.1	U38465	Lycopersicon esculentum	small GTP-binding protein. LeRab1B. ; Ypt1/Rab1A homolog LeRab1B.
BAB07961.1	AP002524	Oryza sativa	putative GTP-binding protein. P0406H10.17. contains ESTs D23874(R0480),AU031678(R0480).
CAA98176.1	Z73948	Lotus japonicus	GTP-binding protein. RAB8E. rab8E.
CAA89021.1	Z49152	Beta vulgaris	GTP-binding. small G protein.
CAA98172.1	Z73944	Lotus japonicus	GTP-binding protein. RAB8A. rab8A.
CAA04701.1	AJ001367	Daucus carota	small GTP-binding protein. Dc-Rab8.
CAA90080.1	Z49900	Pisum sativum	small GTP-binding protein.
AAD46405.1	AF096249	Lycopersicon esculentum	ethylene-responsive small GTP-binding protein. ER43.
CAA98174.1	Z73946	Lotus japonicus	GTP-binding protein. RAB8C. rab8C.
CAA90082.1	Z49902	Pisum sativum	small GTP-binding protein.
CAA49600.1	X69980	Lycopersicon esculentum	GTP-binding protein. ypt2.
CAA98175.1	Z73947	Lotus japonicus	GTP-binding protein. RAB8D. rab8D.
CAA90081.1	Z49901	Pisum sativum	small GTP-binding protein.
AAB17726.1	U38471	Brassica rapa	small GTP-binding protein rab. BRAB-1. small GTP-binding protein rab family.
AAA34251.1	L08128	Volvox carteri	GTP-binding protein. yptV2.
CAA98173.1	Z73945	Lotus japonicus	GTP-binding protein. RAB8B. rab8B.
CAA89049.1	Z49190	Beta vulgaris	GTP-binding. small G protein.
CAA98179.1	Z73951	Lotus japonicus	GTP-binding protein. RAB11C. rab11C.
AAA34253.1	L08130	Volvox carteri	GTP-binding protein. yptV4.

CAA98165.1	Z73937	Lotus japonicus	GTP-binding protein. RAB2A. rab2A.
AAA63902.1	U22433	Zea mays	GTP binding protein. rab2.
AAA90955.1	U32185	Glycine max	vesicular transport. guanine nucleotide regulatory protein. rab2. GTP-binding protein; soyrab.
SEQ ID NO: 628			
AAA87456.1	U22147	Hevea brasiliensis	beta-1,3-glucanase. HGN1. hydrolytic enzyme.
CAB38443.1	AJ133470	Hevea brasiliensis	beta-1,3-glucanase. hgn1.
AAG24921.1	AF311749	Hevea brasiliensis	beta-1,3-glucanase.
AAF44667.1	AF239617	Vitis vinifera	hydrolysis of 1,3-beta-D-glucosidic linkages in 1,3-beta-D-glucans. beta-1,3-glucanase. fungal pathogen defense-related protein.
AAA33648.1	L02212	Pisum sativum	beta-1,3-glucan hydrolysis. beta-1,3-glucanase. putative.
AAB41551.1	U27179	Medicago sativa subsp. sativa	acidic glucanase.
AAB24398.1	S51479	Pisum sativum	beta-1,3-glucanase. beta-1,3-glucanase. This sequence comes from Fig. 1B.
CAA37289.1	X53129	Phaseolus vulgaris	1,3,-beta-D-glucanase.
AAA34078.1	M63634	Nicotiana plumbaginifolia	regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.
AAA51643.1	M23120	Nicotiana plumbaginifolia	beta-glucanase precursor.
CAA30261.1	X07280	Nicotiana plumbaginifolia	beta-glucanase.
AAA03618.1	M80608	Lycopersicon esculentum	beta-1,3-glucanase.
AAC19114.1	AF067863	Solanum tuberosum	1,3-beta-glucan glucanohydrolase. glucanase.
AAA18928.1	U01901	Solanum tuberosum	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). glub2. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAA63539.1	M60402	Nicotiana tabacum	glucan beta-1,3-glucanase. glucanase GLA.
AAA63540.1	M60403	Nicotiana tabacum	glucan-1,3-beta-glucosidase. glucanase GLB.

AAA88794.1	U01900	<i>Solanum tuberosum</i>	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB1. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAA63541.1	M59442	<i>Nicotiana tabacum</i>	basic beta-1,3-glucanase. glucanase.
AAB82772.2	AF001523	<i>Musa acuminata</i>	beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
AAF08679.1	AF004838	<i>Musa acuminata</i>	beta-1,3-glucanase.
AAA19111.1	U01902	<i>Solanum tuberosum</i>	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB3. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAC04710.1	AF034106	<i>Glycine max</i>	beta-1,3-glucanase 1. SGlu1.
AAC04714.1	AF034113	<i>Glycine max</i>	beta-1,3-glucanase 8. SGlu8.
CAB91554.1	AJ277900	<i>Vitis vinifera</i>	beta 1-3 glucanase. gl.
AAA34082.1	M20620	<i>Nicotiana tabacum</i>	prepro-beta-1,3-glucanase precursor.
CAA03908.1	AJ000081	<i>Citrus sinensis</i>	glucan hydrolase. beta-1,3-glucanase. gns1.
AAB03501.1	U41323	<i>Glycine max</i>	beta-1,3-glucanase. SGN1.
AAA92013.1	U49454	<i>Prunus persica</i>	beta-1,3-glucanase. Gns1.
AAA33946.1	M37753	<i>Glycine max</i>	beta-1,3-endoglucanase (EC 3.2.1.39).
AAA63542.1	M59443	<i>Nicotiana tabacum</i>	acidic beta-1,3-glucanase. glucanase.
AAF34761.1	AF227953	<i>Capsicum annuum</i>	basic beta-1,3-glucanase. BGLU.
AAD33881.1	AF141654	<i>Nicotiana tabacum</i>	beta-1,3-glucanase. GGL4.
AAG34080.1	AF294849	<i>Capsicum annuum</i>	beta-1,3-glucanase-like protein.
AAF33405.1	AF230109	<i>Populus x canescens</i>	beta-1,3 glucanase. BGLUC.

AAD33880.1	AF141653	Nicotiana tabacum	beta-1,3-glucanase. GGL1.
CAA57255.1	X81560	Nicotiana tabacum	(1-)-beta-glucanase. Sp41a.
AAA34053.1	M60464	Nicotiana tabacum	beta-1,3-glucanase.
SEQ ID NO: 630			
AAD37698.1	AF145729	Oryza sativa	homeodomain leucine zipper protein. Oshox5. transcription factor.
BAA05624.1	D26575	Daucus carota	transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.
AAF01765.1	AF184278	Glycine max	homeodomain-leucine zipper protein 57. Hdl57. transcription factor.
CAA64417.1	X94947	Lycopersicon esculentum	homeobox. VAHOX1.
BAA93465.1	AB028077	Physcomitrella patens	homeobox protein PpHB6. PpHB6. homeodomain-leucine zipper gene.
BAB18171.1	AB042769	Zinnia elegans	homeobox-leucine zipper protein. ZeHB3. full length.
BAA93460.1	AB028072	Physcomitrella patens	homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.
BAA93466.1	AB028078	Physcomitrella patens	homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.
BAA93461.1	AB028073	Physcomitrella patens	homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.
BAA05625.1	D26576	Daucus carota	transcriptional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.
BAA05622.1	D26573	Daucus carota	transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.
BAA93467.1	AB028079	Physcomitrella patens	homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.
BAA93464.1	AB028076	Physcomitrella patens	homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.
AAD37697.1	AF145728	Oryza sativa	homeodomain leucine zipper protein. Oshox4. transcription factor.
AAF01764.2	AF184277	Glycine max	homeodomain-leucine zipper protein 56. Hdl56. transcription factor.
BAA21017.1	D26578	Daucus carota	transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.

BAB18168.1	AB042766	<i>Zinnia elegans</i>	homeobox-leucine zipper protein. ZeHB7. 3'RACE product.
BAA93468.1	AB028080	<i>Physcomitrella patens</i>	homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.
BAA05623.1	D26574	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.
AAD37699.1	AF145730	<i>Oryza sativa</i>	homeodomain leucine zipper protein. Oshox6. transcription factor.
AAD38144.1	AF139497	<i>Prunus armeniaca</i>	DNA-binding protein. homeobox leucine zipper protein. HBLZP.
AAA63768.2	AF339748	<i>Helianthus annuus</i>	homeobox-leucine zipper protein HAHB-4. Hahb-4.
BAA93463.1	AB028075	<i>Physcomitrella patens</i>	homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.
CAA64491.1	X95193	<i>Pimpinella brachycarpa</i>	transcription activator. homeobox-leucine zipper protein.
CAA64221.1	X94449	<i>Pimpinella brachycarpa</i>	transcription activator. homeobox-leucine zipper protein. PHZ4.
CAA64152.1	X94375	<i>Pimpinella brachycarpa</i>	transcription activator. homeobox-leucine zipper protein.
AAD37700.1	AF145731	<i>Oryza sativa</i>	homeodomain leucine zipper protein. Oshox7. transcription factor.
AAD37695.1	AF145726	<i>Oryza sativa</i>	homeodomain leucine zipper protein. Oshox2. transcription factor.
CAA06728.1	AJ005833	<i>Craterostigma plantagineum</i>	transcription factor. homeodomain leucine zipper protein. hb-2.
CAA62608.1	X91212	<i>Lycopersicon esculentum</i>	HD-ZIP protein. THOM1.
CAA63222.1	X92489	<i>Glycine max</i>	transcription activator. homeobox-leucine zipper protein.
CAA65456.2	X96681	<i>Oryza sativa</i>	transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.
AAF19980.1	AF211193	<i>Oryza sativa</i>	homeodomain-leucine zipper transcription factor. Hox1. hox1.
SEQ ID NO: 631			
CAC19183.1	AJ291816	<i>Cicer arietinum</i>	expansin.
AAD13633.1	AF059489	<i>Lycopersicon esculentum</i>	expansin precursor. Exp5.
AAG13983.1	AF297522	<i>Prunus avium</i>	expansin 2. Exp2. PruavExp2.

AAF35902.1	AF230333	<i>Zinnia elegans</i> expansin 3.
AAF32409.1	AF230276	<i>Triphysaria versicolor</i> alpha-expansin 3.
AAC96080.1	AF049353	<i>Nicotiana tabacum</i> involved in acid-growth response. alpha-expansin precursor. Nt-EXP4. cell wall protein.
AAG13982.1	AF297521	<i>Prunus avium</i> expansin 1. Exp1. PruavExp1.
AAC33529.1	U93167	<i>Prunus armeniaca</i> expansin. PA-Exp1.
AAF32411.1	AF230278	<i>Triphysaria versicolor</i> alpha-expansin 1.
AAF35901.1	AF230332	<i>Zinnia elegans</i> expansin 2.
AAF21101.1	AF159563	<i>Fragaria x ananassa</i> expansin. Exp2. ripening regulated.
BAB19676.1	AB029083	<i>Prunus persica</i> expansin. PchExp1.
AAD47901.1	AF085330	<i>Pinus taeda</i> expansin.
AAC33530.1	AF038815	<i>Prunus armeniaca</i> expansin. Exp2.
CAC19184.1	AJ291817	<i>Cicer arietinum</i> expansin.
AAB40635.1	U64891	<i>Pinus taeda</i> expansin. similar to <i>Arabidopsis</i> expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to <i>Cucumis sativus</i> expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAG32921.1	AF184233	<i>Lycopersicon esculentum</i> expansin. Exp10.
AAD49956.1	AF167360	<i>Rumex palustris</i> expansin. EXP1.
AAB40637.1	U64893	<i>Pinus taeda</i> expansin. similar to <i>Arabidopsis</i> expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to <i>Cucumis sativus</i> expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAB40634.1	U64890	<i>Pinus taeda</i> expansin. similar to <i>Arabidopsis</i> expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to <i>Cucumis sativus</i> expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAB37746.1	U30382	Cucumis sativus	expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.
AAB40636.1	U64892	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAC39512.1	AF043284	Gossypium hirsutum	expansin. GhEX1. contains N-terminal signal peptide.
CAB43197.1	AJ239068	Lycopersicon esculentum	cell wall loosening enzyme. expansin2. exp2.
AAC64201.1	AF096776	Lycopersicon esculentum	expansin. LeEXP2.
AAC96081.1	AF049354	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.
CAB46492.1	AJ243340	Lycopersicon esculentum	expansin9. exp9.
AAF17570.1	AF202119	Marsilea quadrifolia	alpha-expansin. EXP1. Mq-EXP1.
AAB81662.1	U85246	Oryza sativa	expansin. Os-EXP4.
AAF62180.1	AF247162	Oryza sativa	alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.
AAB38074.1	U30477	Oryza sativa	induces extension (creep) in plant cell walls. expansin Os-EXP2. Os-EXP2. former gene name RiExB.
AAD13632.1	AF059488	Lycopersicon esculentum	expansin precursor. Exp4.
AAF32410.1	AF230277	Triphysaria versicolor	alpha-expansin 2.
AAG01875.1	AF291659	Striga asiatica	alpha-expansin 3. Exp3.
CAA04385.1	AJ000885	Brassica napus	Cell wall extension in plants. Expansin.
CAA06271.2	AJ004997	Lycopersicon esculentum	expansin18. exp18.
BAB32732.1	AB049406	Eustoma grandiflorum	expansin. Eg Expansin.
AAC63088.1	U82123	Lycopersicon esculentum	expansin. LeEXP1. fruit ripening regulated expansin.



AAF62182.1	AF247164	Oryza sativa	alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.
AAB37749.1	U30460	Cucumis sativus	expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
AAG32920.1	AF184232	Lycopersicon esculentum	expansin. Exp8.
CAC06433.1	AJ276007	Festuca pratensis	expansin. exp2.
AAF62181.1	AF247163	Oryza sativa	alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.
AAC96079.1	AF049352	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.
AAC96077.1	AF049350	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
BAA88200.1	AP000837	Oryza sativa	EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
AAF17571.1	AF202120	Regnellidium diphyllum	alpha-expansin. EXP1. Rd-EXP1.
AAC96078.1	AF049351	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
AAG01874.1	AF291658	Striga asiatica	alpha-expansin 2. Exp2.
SEQ ID NO: 634			
AAF63205.1	AF245119	Mesembryanthemum crystallinum	AP2-related transcription factor. CDBP. stress induced transcription factor.
BAA97122.1	AB016264	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
BAA07321.1	D38123	Nicotiana tabacum	ERF1. ethylene-responsive transcription factor.
AAG43545.1	AF211527	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
BAA87068.1	AB035270	Matricaria chamomilla	ethylene-responsive element binding protein1 homolog. McEREBP1.
BAA97124.1	AB016266	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
AAC62619.1	AF057373	Nicotiana tabacum	transcription factor. ethylene response element binding protein 1. EREBP1.
CAB93940.1	AJ238740	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca2.

AAK31279.1	AC079890	Oryza sativa	putative ethylene-responsive element binding protein. OSJNBb0089A17.16.
AAG60182.1	AC084763	Oryza sativa	putative ethylene-responsive element binding protein. OSJNBa0027P10.12.
CAB96900.1	AJ251250	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
CAB96899.1	AJ251249	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
CAC12822.1	AJ299252	Nicotiana tabacum	AP2 domain-containing transcription factor. ap2.
AAF23899.1	AF193803	Oryza sativa	transcription factor EREBP1. EREBP/AP2-like transcription factor.
AAF05606.1	AF190770	Oryza sativa	EREBP-like protein. tsh1. TSH1; induced by ethylene.
BAA97123.1	AB016265	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
BAA76734.1	AB024575	Nicotiana tabacum	ethylene responsive element binding factor.
BAB03248.1	AB037183	Oryza sativa	ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
CAB93939.1	AJ238739	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca1.
AAD00708.1	U91857	Stylosanthes hamata	ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
AAG43548.1	AF211530	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
AAG43549.1	AF211531	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
AAK31271.1	AC079890	Oryza sativa	putative transcriptional factor. OSJNBb0089A17.22.
AAK01088.1	AF298230	Hordeum vulgare	CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
AAC49567.1	U41466	Zea mays	Glossy15. Glossy15. AP2 DNA-binding domain protein; similar to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.
SEQ ID NO: 635			
CAC19789.1	AJ251686	Catharanthus roseus	putative transcription factor. MYB-like DNA-binding protein. bpf-1.

CAA55693.1	X79086	Zea mays	initiator-binding protein. IBP2.
CAA55691.1	X79085	Zea mays	initiator binding protein. IBP1.
AAF97508.1	AF242298	Oryza sativa	telomere binding protein-1. TBP1.
SEQ ID NO: 636			
CAB43505.1	AJ239051	Cicer arietinum	cytochrome P450. cyp81E2.
BAA22422.1	AB001379	Glycyrrhiza echinata	cytochrome P450. CYP81E1.
BAA74465.1	AB022732	Glycyrrhiza echinata	cytochrome P450. CYP Ge-31.
CAA10067.1	AJ012581	Cicer arietinum	cytochrome P450. cyp81E3.
CAB41490.1	AJ238439	Cicer arietinum	cytochrome P450 monooxygenase. cyp81E3v2.
BAA93634.1	AB025016	Lotus japonicus	cytochrome P450.
CAA04117.1	AJ000478	Helianthus tuberosus	fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11. chimeric sequence (from 5'-race).
CAA04116.1	AJ000477	Helianthus tuberosus	fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
AAK38080.1	AF321856	Lolium rigidum	putative cytochrome P450.
AAK38079.1	AF321855	Lolium rigidum	putative cytochrome P450.
AAK38081.1	AF321857	Lolium rigidum	putative cytochrome P450.
AAC34853.1	AF082028	Hemerocallis hybrid cultivar	putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3. mRNA accumulates in senescing petals.
CAA65580.1	X96784	Nicotiana tabacum	cytochrome P450. hsr515.
CAB56742.1	AJ249800	Cicer arietinum	cytochrome P450 monooxygenase. cyp81E5.
AAA32913.1	M32885	Persea americana	cytochrome P-450LXXIA1 (cyp71A1).
BAA12159.1	D83968	Glycine max	Cytochrome P-450 (CYP93A1).
AAD56282.1	AF155332	Petunia x hybrida	flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

CAA71515.1	Y10491	Glycine max putative cytochrome P450.
AAB94590.1	AF022461	Glycine max CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
CAA71516.1	Y10492	Glycine max putative cytochrome P450.
CAA64635.1	X95342	Nicotiana tabacum cytochrome P450. hsr515. hypersensitivity-related gene.
BAA13076.1	D86351	Glycine max cytochrome P-450 (CYP93A2).
AAG44132.1	AF218296	Pisum sativum cytochrome P450. P450 isolog.
AAG09208.1	AF175278	Pisum sativum wound-inducible P450 hydroxylase. CYP82A1.
AAC49188.2	U29333	Pisum sativum cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
AAD38930.1	AF135485	Glycine max cytochrome P450 monooxygenaseCYP93D1. CYP93E1.
CAA71876.1	Y10982	Glycine max putative cytochrome P450.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
CAA70576.1	Y09424	Nepeta racemosa cytochrome P450. CYP71A6.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
CAA71877.1	Y10983	Glycine max putative cytochrome P450.
AAB94587.1	AF022458	Glycine max CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAC39454.1	AF014802	Eschscholzia californica (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome P-450-dependent, homologous to wound-inducible CYP82A1 of Pisum sativum GenBank Accession Number U29333.
BAA92894.1	AB006790	Petunia x hybrida cytochrome P450. IMT-2.
BAA84072.1	AB028152	Torenia hybrida flavone synthase II. cytochrome P450. TFNS5.
BAA35080.1	AB015762	Nicotiana tabacum putative cytochrome P450. CYP82E1.
CAB56743.1	AJ249801	Cicer arietinum cytochrome P450 monooxygenase. cyp81E4.

AAB17562.1	U72654	<i>Eustoma grandiflorum</i> flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
AAG34695.1	AF313492	<i>Matthiola incana</i> putative cytochrome P450.
BAA74466.1	AB022733	<i>Glycyrrhiza echinata</i> cytochrome P450. CYP Ge-51.
BAA22423.1	AB001380	<i>Glycyrrhiza echinata</i> cytochrome P450. CYP93B1.
SEQ ID NO: 639		
AAC06319.1	AF053084	<i>Malus x domestica</i> putative cinnamyl alcohol dehydrogenase. CAD.
CAA61275.1	X88797	<i>Eucalyptus gunnii</i> cinnamyl alcohol dehydrogenase. CAD1.
SEQ ID NO: 640		
BAA92916.1	AP001539	<i>Oryza sativa</i> EST C26826(C50159) corresponds to a region of the predicted gene. Similar to <i>Arabidopsis thaliana</i> chromosome II BAC F13A10; putative ARF1 family auxin responsive transcription factor. (AC006418).
AAK21342.1	AC024594	<i>Oryza sativa</i> putative transcription factor. OSJNBa0093B11.2.
AAG43286.1	AF140228	<i>Oryza sativa</i> auxin response factor 1.
SEQ ID NO: 641		
CAC24691.1	AJ132363	<i>Brassica juncea</i> efflux carrier of polar auxin transport. pina.
AAG17172.1	AF190881	<i>Populus tremula x Populus tremuloides</i> PIN1-like auxin transport protein. ppl1.
AAC39514.1	AF056027	<i>Oryza sativa</i> auxin transport protein REH1. REH1. potential membrane protein.
SEQ ID NO: 642		
AAG22044.1	AF305783	<i>Pisum sativum</i> apyrase 2. apy2. phosphatase.
AAF00610.1	AF156781	<i>Dolichos biflorus</i> apyrase. apyrase-2.
AAG32959.1	AF207687	<i>Glycine soja</i> apyrase GS50.
AAG32960.1	AF207688	<i>Glycine soja</i> apyrase GS52.
AAF00609.1	AF156780	<i>Lotus japonicus</i> apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
AAD31285.1	AF139807	<i>Dolichos biflorus</i> apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.

AAF00611.1	AF156782	Medicago sativa	apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
AAK15160.1	AF288132	Medicago truncatula	putative apyrase. apy1. nucleotide phosphohydrolase; Mtapy1.
BAB18896.1	AB038669	Pisum sativum	apyrase.
BAB18895.1	AB038668	Pisum sativum	apyrase.
BAB18894.1	AB038555	Pisum sativum	apyrase H-type.
BAB18893.1	AB038554	Pisum sativum	apyrase S-type.
BAB18900.1	AB027614	Pisum sativum	apyrase.
BAB40230.1	AB027613	Pisum sativum	S-type apyrase. ATP diphosphohydrolase (apyrase) S-type.
BAB18890.1	AB023621	Pisum sativum	apyrase S-type. ATP diphosphohydrolase (apyrase) S-type.
BAA75506.1	AB022319	Pisum sativum	apyrase. cytoskeleton associated.
BAA89275.1	AB027616	Pisum sativum	apyrase.
BAB40231.1	AB027615	Pisum sativum	S-type apyrase. ATP diphosphohydrolase (apyrase) S-type.
AAB02720.1	U58597	Solanum tuberosum	catalyzes the hydrolysis of phosphoanhydride bonds of nucleoside tri- and di- phosphates in the presence of divalent cations. ATP-diphosphohydrolase. RROP1. apyrase, Ecto-ATPase, E-type ATPase; NTP-diphosphohydrolase.
AAK15161.1	AF288133	Medicago truncatula	putative apyrase. apy4. nucleotide phosphohydrolase; Mtapy4.
BAB18891.1	AB030444	Pisum sativum	apyrase. ATP diphosphohydrolase, (EC 3.6.1.5) this sequence is reported in Acc#:AB022319.
BAB18892.1	AB030445	Pisum sativum	apyrase. ATP diphosphohydrolase, EC 3.6.1.5 this sequence is reported in Acc#:AB022319, Acc#:AB027613.
SEQ ID NO: 645			
AAG22044.1	AF305783	Pisum sativum	apyrase 2. apy2. phosphatase.
AAF00610.1	AF156781	Dolichos biflorus	apyrase. apyrase-2.
AAG32959.1	AF207687	Glycine soja	apyrase GS50.

AAG32960.1	AF207688	Glycine soja apyrase GS52.
AAD31285.1	AF139807	Dolichos biflorus apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
AAK15160.1	AF288132	Medicago truncatula putative apyrase. apyl. nucleotide phosphohydrolase; Mtapyl.
AAF00609.1	AF156780	Lotus japonicus apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
BAB18896.1	AB038669	Pisum sativum apyrase.
BAB18895.1	AB038668	Pisum sativum apyrase.
BAB18894.1	AB038555	Pisum sativum apyrase H-type.
BAB18893.1	AB038554	Pisum sativum apyrase S-type.
BAB18900.1	AB027614	Pisum sativum apyrase.
BAB40230.1	AB027613	Pisum sativum S-type apyras. ATP diphosphohydrolase (apyrase) S-type.
BAB18890.1	AB023621	Pisum sativum apyrase S-type. ATP diphosphohydrolase (apyrase) S-type.
BAA75506.1	AB022319	Pisum sativum apyrase. cytoskeleton associated.
AAF00611.1	AF156782	Medicago sativa apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
BAA89275.1	AB027616	Pisum sativum apyrase.
BAB40231.1	AB027615	Pisum sativum S-type apyrase. ATP diphosphohydrolase (apyrase) S-type.
AAB02720.1	U58597	Solanum tuberosum catalyzes the hydrolysis of phosphoanhydride bonds of nucleoside tri- and di- phosphates in the presence of divalent cations. ATP-diphosphohydrolase. RROP1. apyrase, Ecto-ATPase, E-type ATPase; NTP-diphosphohydrolase.
AAK15161.1	AF288133	Medicago truncatula putative apyrase. apy4. nucleotide phosphohydrolase; Mtapyl4.
BAB18891.1	AB030444	Pisum sativum apyrase. ATP diphosphohydrolase, (EC 3.6.1.5) this sequence is reported in Acc#:AB022319.
BAB18892.1	AB030445	Pisum sativum apyrase. ATP diphosphohydrolase, EC 3.6.1.5 this sequence is reported in Acc#:AB022319, Acc#:AB027613.

SEQ ID NO: 646

AAB80947.1	AF022915	Triticum aestivum	ornithine/acetylornithine aminotransferase.
CAA69936.1	Y08680	Alnus glutinosa	acetylornithine aminotransferase. ag118.
AAK11219.1	AF324485	Oryza sativa	aminotransferase-like protein.
AAG09278.1	AF177590	Vitis vinifera	ornithine aminotransferase.
AAC78480.1	AF085149	Capsicum chinense	putative aminotransferase. pyridoxal phosphate dependent.
AAA02916.1	L08400	Vigna aconitifolia	production of pyrroline-5-carboxylate by deamination of ornithine. ornithine aminotransferase.
AAB59330.1	M31545	Hordeum vulgare	glutamate 1-semialdehyde aminotransferase. GSA. precursor.
AAA18861.1	U03632	Chlamydomonas reinhardtii	glutamate-1-semialdehyde aminotransferase. gsa.
AAA33968.1	L12453	Glycine max	catalyzes 5-aminolevulinic acid formation from GSA. glutamate 1-semialdehyde aminotransferase. Gsa. putative.
AAC48996.1	U20260	Glycine max	converts GSA to 5-aminolevulinic acid. glutamate 1-semialdehyde aminotransferase. Gsa1.
SEQ ID NO: 650			
AAF66982.1	AF247646	Zea mays	transposase. similar to Mutator family transposases.
SEQ ID NO: 652			
AAB41812.1	L36158	Medicago sativa	peroxidase. pxdD. amino acid feature: conserved domains, aa 120 .. 126, 188 .. 195; amino acid feature: heme-binding domain, aa 63 .. 68.
CAA71495.1	Y10469	Spinacia oleracea	peroxidase. prxr8.
CAA09881.1	AJ011939	Trifolium repens	peroxidase. prx2.
CAA62228.1	X90695	Medicago sativa	peroxidase2. prx2.
AAA98491.1	L36981	Petroselinum crispum	anionic peroxidase.
BAB39281.1	AP002971	Oryza sativa	putative peroxidase. P0537A05.10. contains ESTs D24657(R2329),AU082066(R2329).
AAB02926.1	U59284	Linum usitatissimum	peroxidase. FLXPER3.
BAA77387.1	AB024437	Scutellaria baicalensis	peroxidase 1.



CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
CAA71488.1	Y10462	Spinacia oleracea peroxidase. prxr1.
BAA01950.1	D11337	Vigna angularis peroxidase.
BAA14143.1	D90115	Armoracia rusticana peroxidase isozyme.
CAA71490.1	Y10464	Spinacia oleracea peroxidase. prxr3.
CAB94692.1	AJ242742	Ipomoea batatas Removal of H <sub>2</sub> O <sub>2</sub> , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
BAA92497.1	AP001383	Oryza sativa ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to peroxidase ATP18a. (X98804).
AAC36707.1	AF078691	Manihot esculenta peroxidase.
BAA92422.1	AP001366	Oryza sativa ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to A.thaliana mRNA for peroxidase ATP18a. (X98804).
CAA62226.1	X90693	Medicago sativa peroxidase1B. prx1B.
AAF63024.1	AF244921	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx12 precursor. type III peroxidase.
AAA32676.1	M37637	Arachis hypogaea cationic peroxidase. PNC2.
BAA11853.1	D83225	Populus nigra peroxidase.
CAC21393.1	AJ401276	Zea mays peroxidase. pox3.
AAA65636.1	L13653	Lycopersicon esculentum peroxidase. TPX2.
CAB67121.1	Y19023	Lycopersicon esculentum peroxidase. cevi-1.
CAA62227.1	X90694	Medicago sativa peroxidase1C. prx1C.
CAA50597.1	X71593	Lycopersicon esculentum peroxidase. CEVI-1.
AAD37376.1	AF145350	Glycine max peroxidase. Prx4.
AAB67737.1	L77080	Stylosanthes humilis cationic peroxidase.

CAA71489.1	Y10463	Spinacia oleracea peroxidase. prxr2.
CAA71496.1	Y10470	Spinacia oleracea peroxidase. prxr9.
CAA71494.1	Y10468	Spinacia oleracea peroxidase. prxr7.
BAA06334.1	D30652	Populus kitakamiensis peroxidase.
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA94962.1	AB042103	Asparagus officinalis peroxidase. AspPOX1.
CAA80502.1	Z22920	Spirodela polyrrhiza peroxidase.
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA11852.1	D83224	Populus nigra peroxidase.
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA07241.1	D38051	Populus kitakamiensis peroxidase. prxA4a.
AAD11481.1	U51191	Glycine max peroxidase precursor. sEPa1.
AAC98519.1	AF007211	Glycine max peroxidase precursor. GMIPER1. pathogen-induced.
AAA32973.1	M73234	Hordeum vulgare peroxidase BP 1. Prx5.
AAB47602.1	L07554	Linum usitatissimum peroxidase. FLXPER1.
AAB41810.1	L36156	Medicago sativa peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
AAF63027.1	AF244924	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
AAA34108.1	J02979	Nicotiana tabacum lignin-forming peroxidase precursor (EC 1.11.1.7).
AAD43561.1	AF155124	Gossypium hirsutum bacterial-induced peroxidase precursor. Perx_Goshiko.
SEQ ID NO: 653		

AAB97617.1	U83687	<i>Apium graveolens</i>	NADPH-dependent mannose 6-phosphate reductase. m6pr. aldo-keto reductase; similar to aldose 6-phosphate reductase also known as NADP-sorbitol-6-phosphate dehydrogenase encoded by GenBank Accession Number D11080.
BAA01853.1	D11080	<i>Malus x domestica</i>	NADP-dependent D-sorbitol-6-phosphate dehydrogenase. S6PDH.
AAC97607.1	AF057134	<i>Malus x domestica</i>	synthesizes sorbitol, a major photosynthetic product in many members of the Rosaceae family. NADP-dependent sorbitol 6-phosphate dehydrogenase. S6PDH.
SEQ ID NO: 654			
BAA82556.1	AB030083	<i>Populus nigra</i>	lectin-like protein kinase. PnLPK.
AAB61708.1	U93048	<i>Daucus carota</i>	somatic embryogenesis receptor-like kinase. SERK.
BAB19337.1	AP003044	<i>Oryza sativa</i>	putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
AAK21965.1	AY028699	<i>Brassica napus</i>	receptor protein kinase PERK1.
BAB39873.1	AP002882	<i>Oryza sativa</i>	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAB93834.1	U82481	<i>Zea mays</i>	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
BAB18292.1	AP002860	<i>Oryza sativa</i>	putative receptor-like protein kinase. P0409B08.19.
AAK00425.1	AC069324	<i>Oryza sativa</i>	Putative protein kinase. OSJNBa0071K19.11.
AAD21872.1	AF078082	<i>Phaseolus vulgaris</i>	receptor-like protein kinase homolog RK20-1.
AAC23542.1	U20948	<i>Ipomoea trifida</i>	receptor protein kinase. IRK1.
CAA73134.1	Y12531	<i>Brassica oleracea</i>	serine/threonine kinase. BRLK.
CAB51480.1	Y14600	<i>Sorghum bicolor</i>	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
AAG59657.1	AC084319	<i>Oryza sativa</i>	putative protein kinase. OSJNBa0004B24.20.
BAB16871.1	AP002537	<i>Oryza sativa</i>	putative protein kinase APK1A <i>Arabidopsis thaliana</i> . P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.
BAA94517.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
CAB51836.1	AJ243961	Oryza sativa	Putitive Ser/Thr protein kinase. 11332.7.
BAA78764.1	AB023482	Oryza sativa	ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
AAF91324.1	AF244890	Glycine max	receptor-like protein kinase 3. RLK3. GmRLK3.

CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
BAA92953.1	AP001551	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).
BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
BAB07906.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.14.
BAA94516.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
SEQ ID NO: 655			
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.

CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrk1.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.

AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAA94529.2	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).
AAF34428.1	AF172282	Oryza sativa	receptor-like protein kinase. DUPR11.18.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461), C22360(C11461).
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAA94516.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
BAB07906.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.14.
SEQ ID NO: 657			
AAF43869.1	AF166114	Chloroplast Mesostigma viride	probable transport protein. cysA.
BAB17113.1	AP002866	Oryza sativa	putative white protein; ATP-binding cassette transporter. P0410E01.34.
BAA57907.1	AB001684	Chlorella vulgaris	sulfate transport system permease protein. cysA.
AAD54843.1	AF137379	Chloroplast Nephroselmis olivacea	probable transport protein. cysA.
BAA90508.1	AP001111	Oryza sativa	similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAA90507.1	AP001111	Oryza sativa	similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAA83352.1	AP000391	Oryza sativa	ESTs AU067992(C11433), AU077424(C11433) correspond to a region of the predicted gene.; Similar to ABC transporter-7 (U43892).
AAG49003.1	AY013246	Hordeum vulgare	putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and comparative sequence.
AAD10836.1	U52079	Solanum tuberosum	P-glycoprotein. pmdr1. binds ATP; ATPase; transporter; transmembrane protein.

BAA96612.1	AP002482	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2, BAC F14M4 ; putative ABC transporter (AC004411).
BAB40032.1	AP003046	Oryza sativa	putative ABC transporter. P0445D12.3.
AAG45492.1	AY013245	Oryza sativa	3615.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and comparative sequence.
AAG49002.1	AY013246	Hordeum vulgare	putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative sequencing.
BAB21275.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.6.
BAB21273.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.4.
CAA94437.1	Z70524	Spirodela polyrrhiza	multidrug resistance protein. PDR5-like ABC transporter.
BAB21276.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
BAB21279.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.10. contains ESTs AU065360(R3463),AU101680(R3463).
SEQ ID NO: 658			
AAD10386.1	U72255	Oryza sativa	beta-1,3-glucanase precursor. Gns9.
BAA89481.1	AB029462	Salix gilgiana	beta-1,3-glucanase. SgGN1.
CAB85903.1	AJ251646	Pisum sativum	hydrolysis of beta-1,3 conjugated glucans. beta-1,3 glucanase. gns2.
CAA49513.1	X69887	Brassica napus	beta-1,3-glucanase homologue.
AAA90953.1	U30323	Triticum aestivum	beta 1,3-glucanase. Glc1.
BAB19363.1	AP002542	Oryza sativa	putative beta-1,3-glucanase. P0679C08.2.
CAA82271.1	Z28697	Nicotiana tabacum	beta-1,3-glucanase.
CAA30261.1	X07280	Nicotiana plumbaginifolia	beta-glucanase.
AAA51643.1	M23120	Nicotiana plumbaginifolia	beta-glucanase precursor.
AAA34078.1	M63634	Nicotiana plumbaginifolia	regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.



AAB82772.2	AF001523	<i>Musa acuminata</i>	beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
AAF08679.1	AF004838	<i>Musa acuminata</i>	beta-1,3-glucanase.
CAB71021.1	AJ271598	<i>Hieracium piloselloides</i>	putative role in callose degradation. putative beta-1,3-glucanase. gluc.
AAD10383.1	U72252	<i>Oryza sativa</i>	beta-1,3-glucanase precursor. Gns6.
AAD28732.1	AF112965	<i>Triticum aestivum</i>	beta-1,3-glucanase precursor. Glb3.
BAB40807.1	AB052291	<i>Pyrus pyrifolia</i>	catalyzing the hydrolysis of 1,3-beta-glucosyl linkages. endo-1,3-beta-glucanase-like protein. bgn-1. Amino acid alignment of the protein(BGN-1) encoded by pear pollen bgn-1 with barley endo-1,3-beta-glucanase(GIL. accession number: pdb/1GHS-B/2.3/2/306/N/)(40% identity) and their hydrophobic cluster analysis(HCA)(a overall HCA homology score of 87.1%) showed that it was most likely that the bgn-1 encoded a endo-1,3-beta-glucanase. A higher identity(59.3%) was found between BGN-1 and a putative pea endo-1,3-beta-glucanase (accession number: dad/AJ251646-1).
AAA63539.1	M60402	<i>Nicotiana tabacum</i>	glucan beta-1,3-glucanase. glucanase GLA.
AAA63541.1	M59442	<i>Nicotiana tabacum</i>	basic beta-1,3-glucanase. glucanase.
AAA63540.1	M60403	<i>Nicotiana tabacum</i>	glucan-1,3-beta-glucosidase. glucanase GLB.
AAA32939.1	M62907	<i>Hordeum vulgare</i>	hydrolysis of beta-(1-3)-glucan. (1-3)-beta-glucanase. cBGL32.
AAC14399.1	AF030771	<i>Hordeum vulgare</i>	beta-1,3-glucanase 2. BGL32.
AAA87456.1	U22147	<i>Hevea brasiliensis</i>	beta-1,3-glucanase. HGN1. hydrolytic enzyme.
BAA77784.1	AB027429	<i>Oryza sativa</i>	beta-1,3-glucanase.
BAA77785.1	AB027430	<i>Oryza sativa</i>	beta-1,3-glucanase.
CAB91554.1	AJ277900	<i>Vitis vinifera</i>	beta 1-3 glucanase. gl.
AAD10381.1	U72250	<i>Oryza sativa</i>	beta-1,3-glucanase precursor. Gns4.
AAA33946.1	M37753	<i>Glycine max</i>	beta-1,3-endoglucanase (EC 3.2.1.39).
AAD33881.1	AF141654	<i>Nicotiana tabacum</i>	beta-1,3-glucanase. GGL4.

AAB86541.1	AF030166	Oryza sativa	glucanase. glu1.
AAD10384.1	U72253	Oryza sativa	beta-1,3-glucanase precursor. Gns7.
CAB38443.1	AJ133470	Hevea brasiliensis	beta-1,3-glucanase. hgn1.
AAB03501.1	U41323	Glycine max	beta-1,3-glucanase. SGN1.
AAA18928.1	U01901	Solanum tuberosum	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). glub2. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAA88794.1	U01900	Solanum tuberosum	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB1. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAC19114.1	AF067863	Solanum tuberosum	1,3-beta-glucan glucanohydrolase. glucanase.
AAG24921.1	AF311749	Hevea brasiliensis	beta-1,3-glucanase.
CAA03908.1	AJ000081	Citrus sinensis	glucan hydrolase. beta-1,3-glucanase. gns1.
CAA37289.1	X53129	Phaseolus vulgaris	1,3,-beta-D-glucanase.
CAA57255.1	X81560	Nicotiana tabacum	(1-)-beta-glucanase. Sp41a.
SEQ ID NO: 659			
AAB65776.1	U97521	Vitis vinifera	class IV endochitinase. VvChi4A.
AAB65777.1	U97522	Vitis vinifera	class IV endochitinase. VvChi4B.
BAA03751.1	D16223	Oryza sativa	endochitinase. Cht-3.
CAA30142.1	X07130	Solanum tuberosum	endochitinase.
BAA03749.1	D16221	Oryza sativa	endochitinase. Cht-1.
SEQ ID NO: 660			
AAF07221.1	AF072519	Nicotiana tabacum	centrin. CEN1. caltractin; EF-hand domain calcium-binding protein.

AAF07222.1	AF072520	Nicotiana tabacum	centrin. CEN2. caltractin; EF-hand domain calcium-binding protein.
CAA49153.1	X69220	Scherffelia dubia	caltractin.
AAC04626.1	U92973	Marsilea vestita	calcium-binding protein. centrin. MvCen1. caltractin.
AAB67855.1	U53812	Dunaliella salina	caltractin-like protein.
CAA41039.1	X57973	Chlamydomonas reinhardtii	caltractin.
CAA31163.1	X12634	Chlamydomonas reinhardtii	caltractin (AA 1 - 169).
SEQ ID NO: 664			
BAB16432.1	AB041520	Nicotiana tabacum	WRKY transcription factor Nt-SubD48. Nt-SubD48.
AAC49528.1	U56834	Petroselinum crispum	DNA-binding. WRKY3. WRKY-type DNA-binding protein.
AAD27591.1	AF121354	Petroselinum crispum	binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.
AAD32676.1	AF140553	Avena sativa	DNA-binding protein WRKY3. wrky3. putative transcription factor.
BAA77358.1	AB020023	Nicotiana tabacum	WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.
AAG46150.1	AC018727	Oryza sativa	putative DNA-binding protein. OSJNBa0056G17.18.
BAB40073.1	AP003074	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
BAB18313.1	AP002865	Oryza sativa	putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
AAD38283.1	AC007789	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAA77383.1	AB020590	Nicotiana tabacum	transcription factor NtWRKY2.
BAA82107.1	AB022693	Nicotiana tabacum	transcription factor. NtWRKY1.
CAA88326.1	Z48429	Avena fatua	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAD32677.1	AF140554	Avena sativa	DNA-binding protein WRKY1. wrky1. putative transcription factor.
AAD55974.1	AF121353	Petroselinum crispum	zinc-finger type transcription factor WRKY1. WRKY1.

AAC49529.1	U58540	<i>Petroselinum crispum</i>	WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
AAC49527.1	U48831	<i>Petroselinum crispum</i>	WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.
AAC31956.1	AF080595	<i>Pimpinella brachycarpa</i>	zinc finger protein. ZFP1. WRKY1.
BAA86031.1	AB026890	<i>Nicotiana tabacum</i>	transcription factor NtWRKY4.
AAD16139.1	AF096299	<i>Nicotiana tabacum</i>	DNA-binding protein 2. WRKY2. transcription factor.
AAF23898.1	AF193802	<i>Oryza sativa</i>	zinc finger transcription factor WRKY1.
AAD16138.1	AF096298	<i>Nicotiana tabacum</i>	DNA-binding protein 1. WRKY1. transcription factor.
AAC37515.1	L44134	<i>Cucumis sativus</i>	SPF1-like DNA-binding protein.
AAG35658.1	AF204925	<i>Petroselinum crispum</i>	transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.
CAA88331.1	Z48431	<i>Avena fatua</i>	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
BAB19075.1	AP002744	<i>Oryza sativa</i>	putative DNA-binding protein homolog. P0006C01.17.
BAB19096.1	AP002839	<i>Oryza sativa</i>	putative DNA-binding protein homolog. P0688A04.2.
AAK16170.1	AC079887	<i>Oryza sativa</i>	putative DNA binding protein. OSJNBa0040E01.4.
AAK16171.1	AC079887	<i>Oryza sativa</i>	putative DNA-binding protein. OSJNBa0040E01.10.
AAG35659.1	AF204926	<i>Petroselinum crispum</i>	transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.
CAB97004.1	AJ278507	<i>Solanum tuberosum</i>	putative transcription factor. WRKY DNA binding protein. WRKY1.
AAF61864.1	AF193771	<i>Nicotiana tabacum</i>	DNA-binding protein 4. WRKY4. transcription factor.
BAA87069.1	AB035271	<i>Matricaria chamomilla</i>	elicitor-induced DNA-binding protein homolog. McWRKY1.
AAF61863.1	AF193770	<i>Nicotiana tabacum</i>	DNA-binding protein 3. WRKY3. transcription factor.
SEQ ID NO: 665			
AAD02558.1	AF049933	<i>Petunia x hybrida</i>	PGPS/NH17. PGPS/NH17. protein sec61 gamma subunit homolog; protein transport to ER.
SEQ ID NO: 667			

AAD51623.1 AF169020 Glycine max  
seed maturation protein PM35. PM35. similar to Phaseolus vulgaris putative osmoprotector  
PvLEA-18.

AAC49859.1 U72764 Phaseolus vulgaris  
putative osmoprotector. PvLEA-18. Pvlea-18. atypical late embryogenesis abundant protein.

AAF81194.1 AF240774 Phaseolus vulgaris  
LEA-18.

SEQ ID NO: 672

CAB40743.1 AJ011885 Solanum tuberosum  
starch branching enzyme II. sbe II.

CAB40746.1 AJ011888 Solanum tuberosum  
starch branching enzyme II. SBE II.

CAB40748.1 AJ011890 Solanum tuberosum  
starch branching enzyme II. SBE II.

AAD30186.1 AF076679 Triticum aestivum  
starch branching enzyme-I. SBE-I.

AAD30187.1 AF076680 Aegilops tauschii  
starch branching enzyme-I. SBE-I.

BAA82348.1 AB029548 Phaseolus vulgaris  
branching enzyme 1. kbe1.

CAA56319.1 X80009 Pisum sativum  
starch branching enzyme I. SBEI.

CAB40747.1 AJ011889 Solanum tuberosum  
starch branching enzyme II. SBE II.

CAA03846.1 AJ000004 Solanum tuberosum  
branches 1,4-alpha glucans. starch branching enzyme II, SBE-II. Sbe-II.

BAA03738.1 D16201 Oryza sativa  
branching enzyme-3 precursor.

AAG27623.1 AF286319 Triticum aestivum  
starch branching enzyme 2. Sbe2. glucosyltransferase.

CAA72154.1 Y11282 Triticum aestivum  
1,4-alpha-glucan branching enzyme II. sbe2.

AAK26821.1 AF338431 Aegilops tauschii  
starch branching enzyme IIa. SBEIIa.

AAK26822.1 AF338432 Triticum aestivum  
starch branching enzyme IIa variant. SBEIIa variant.

AAC33764.1 AF072725 Zea mays  
starch branching enzyme IIb. ae. SBEIIb.

AAA18571.1 L08065 Zea mays  
starch branching enzyme II.

BAA82828.1 AB023498 Oryza sativa  
starch branching enzyme rbe4. RBE4.

AAC69753.1	AF064560	Hordeum vulgare	starch branching enzyme IIa. sbellA.
CAA56320.1	X80010	Pisum sativum	starch branching enzyme II. SBEII.
AAC69754.1	AF064561	Hordeum vulgare	starch branching enzyme IIb. sbellB.
AAC36471.1	AF072724	Zea mays	starch branching enzyme I. sbel. confirmed by partial peptide sequencing.
AAA82735.1	U17897	Zea mays	starch branching enzyme I. sbel.
AAD50279.2	AF169833	Sorghum bicolor	seed starch branching enzyme. SBE.
BAA01854.1	D11081	Zea mays	branching enzyme-I precursor.
CAA49463.1	X69805	Solanum tuberosum	1,4-alpha-glucan branching enzyme. SBE.
CAA70038.1	Y08786	Solanum tuberosum	1,4-alpha-glucan branching enzyme. sbel.
AAB17086.1	U66376	Triticum aestivum	1,4-alpha-D-glucan 6-alpha-D-(1,4-alpha-D-glucanotransferase. branching enzyme.
AAB67316.1	U65948	Zea mays	formation of alpha-1-6 glucosidic linkage in starch biosynthesis. starch branching enzyme IIa. Sbe2a. starch branching enzyme isozyme SBEIIa.
BAB40334.1	AB042937	Ipomoea batatas	starch branching enzyme. IBE.
BAA01584.1	D10752	Oryza sativa	branching enzyme.
AAD28284.1	AF136268	Oryza sativa subsp. japonica	starch-branching enzyme I. Rbel.
BAA01616.1	D10838	Oryza sativa	1,4-alpha-glucan branching enzyme. sbel.
BAA01855.1	D11082	Oryza sativa	branching enzyme-I precursor.
CAB40981.1	AJ237897	Triticum aestivum	starch branching enzyme I. sbel. alternative.
CAB40979.1	AJ237897	Triticum aestivum	starch branching enzyme I. sbel.
CAB40980.1	AJ237897	Triticum aestivum	starch branching enzyme I. sbel. alternative.
AAG27622.1	AF286318	Triticum aestivum	starch branching enzyme 1. SbelA. glucosyltransferase.
CAA54308.1	X77012	Manihot esculenta	1,4-alpha-glucan branching enzyme. SBE.

CAA72987.1	Y12320	Triticum aestivum	starch branching enzyme I. Sbe1.
AAG27621.1	AF286317	Triticum aestivum	starch branching enzyme 1. Sbe1D. glucosyltransferase.
BAA82349.1	AB029549	Phaseolus vulgaris	branching enzyme 3. kbe3.
AAB61925.1	AF002820	Triticum aestivum	starch branching enzyme I. wSBE I-D2.
CAB40749.1	AJ011891	Solanum tuberosum	starch branching enzyme II. SBE II.
CAB40745.1	AJ011887	Solanum tuberosum	starch branching enzyme II. SBE II.
CAB40744.1	AJ011886	Solanum tuberosum	starch branching enzyme II. SBE II.
BAA85762.1	AB028067	Nicotiana tabacum	starch branching enzyme. SBE.
CAA49371.1	X69713	Manihot esculenta	branching enzyme. r-2.
BAB40335.1	AB042940	Ipomoea batatas	starch branching enzyme. IBE.
CAA49370.1	X69712	Manihot esculenta	branching enzyme. r-1.
AAC72336.1	AF064563	Hordeum vulgare	starch branching enzyme IIb. sbeIIb.
SEQ ID NO: 673			
CAA09881.1	AJ011939	Trifolium repens	peroxidase. prx2.
CAA62228.1	X90695	Medicago sativa	peroxidase2. prx2.
CAA71495.1	Y10469	Spinacia oleracea	peroxidase. prxr8.
AAB41812.1	L36158	Medicago sativa	peroxidase. pxdD. amino acid feature: conserved domains, aa 120 .. 126, 188 .. 195; amino acid feature: heme-binding domain, aa 63 .. 68.
BAA77387.1	AB024437	Scutellaria baicalensis	peroxidase 1.
AAF63024.1	AF244921	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx12 precursor. type III peroxidase.
AAD11483.1	U51193	Glycine max	peroxidase. sEPb1.
AAB67737.1	L77080	Stylosanthes humilis	cationic peroxidase.

BAA07663.1	D42064	Nicotiana tabacum	cationic peroxidase isozyme 38K precursor.
BAA07664.1	D42065	Nicotiana tabacum	cationic peroxidase isozyme 40K precursor.
CAB94692.1	AJ242742	Ipomoea batatas	Removal of H <sub>2</sub> O <sub>2</sub> , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
CAB67121.1	Y19023	Lycopersicon esculentum	peroxidase. cevi-1.
CAA62226.1	X90693	Medicago sativa	peroxidase1B. prx1B.
CAA50597.1	X71593	Lycopersicon esculentum	peroxidase. CEVI-1.
AAD11481.1	U51191	Glycine max	peroxidase precursor. sEPa1.
AAD11484.1	U51194	Glycine max	peroxidase. sEPb2.
BAA82306.1	AB027752	Nicotiana tabacum	peroxidase.
AAA65637.1	L13654	Lycopersicon esculentum	peroxidase. TPX1.
AAD11482.1	U51192	Glycine max	peroxidase precursor. sEPa2.
CAA62225.1	X90692	Medicago sativa	peroxidase1A. prx1A.
AAC98519.1	AF007211	Glycine max	peroxidase precursor. GMIPER1. pathogen-induced.
AAD37427.1	AF149277	Phaseolus vulgaris	peroxidase 1 precursor. FBP1. secretory peroxidase.
BAA14144.1	D90116	Armoracia rusticana	peroxidase isozyme.
AAA98491.1	L36981	Petroselinum crispum	anionic peroxidase.
CAA71488.1	Y10462	Spinacia oleracea	peroxidase. prxr1.
AAD43561.1	AF155124	Gossypium hirsutum	bacterial-induced peroxidase precursor. Perx_Goshiko.
BAA14143.1	D90115	Armoracia rusticana	peroxidase isozyme.
CAA71490.1	Y10464	Spinacia oleracea	peroxidase. prxr3.
AAB02554.1	L37790	Stylosanthes humilis	cationic peroxidase.



CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA01877.1	D11102	Populus kitakamiensis peroxidase. prxA1.
CAA62227.1	X90694	Medicago sativa peroxidase1C. prx1C.
BAA07241.1	D38051	Populus kitakamiensis peroxidase. prxA4a.
BAA01950.1	D11337	Vigna angularis peroxidase.
AAF65464.2	AF247700	Oryza sativa peroxidase POC1.
AAF63027.1	AF244924	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
CAC21393.1	AJ401276	Zea mays peroxidase. pox3.
CAA59487.1	X85230	Triticum aestivum peroxidase. pox4.
AAD37430.1	AF149280	Phaseolus vulgaris peroxidase 5 precursor. FBP5. secretory peroxidase.
CAA71491.1	Y10465	Spinacia oleracea peroxidase. prxr4.
AAB41811.1	L36157	Medicago sativa peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.
BAA03644.1	D14997	Oryza sativa peroxidase.
AAA32676.1	M37637	Arachis hypogaea cationic peroxidase. PNC2.
CAA71494.1	Y10468	Spinacia oleracea peroxidase. prxr7.
AAA34050.1	M74103	Nicotiana sylvestris anionic peroxidase.
CAA40796.1	X57564	Armoracia rusticana peroxidase. peroxidase precursor.
SEQ ID NO: 674		
AAG31438.1	AF241793	Perilla frutescens limonene synthase.
BAA08367.1	D49368	Perilla frutescens limonene cyclase.
BAA21629.1	AB005744	Perilla frutescens catalyzing the cyclization of geranyl pyrophosphate to 1-limonene. 1-limonene synthase. gPFLC. similar to perilla PFLC-1:DDBJ Acc#D49368.

AAG31437.1	AF241792	<i>Perilla frutescens</i> limonene synthase.
AAK06663.1	AF317695	<i>Perilla frutescens</i> var. <i>frutescens</i> limonene synthase.
AAG31435.1	AF241790	<i>Perilla citriodora</i> limonene synthase.
AAF65545.1	AF233894	<i>Perilla citriodora</i> limonene synthase.
AAD50304.1	AF175323	<i>Mentha longifolia</i> limonene synthase. monoterpene synthase.
AAC37366.1	L13459	<i>Mentha spicata</i> 4S-limonene synthase.
AAG01140.1	AF282875	<i>Schizonepeta tenuifolia</i> (+)-4R-limonene synthase.
AAC61260.1	AF061285	<i>Capsicum annuum</i> sesquiterpene cyclase. UV induced.
AAG09949.1	AF171216	<i>Lycopersicon esculentum</i> vetispiradiene synthase. LEVS2. sesquiterpene cyclase.
AAF74977.1	AF270425	<i>Gossypium hirsutum</i> (E,E)-farnesyl diphosphate cyclase. (+)-delta-cadinene synthase. cdn2. sesquiterpene cyclase.
BAA82141.1	AB023816	<i>Solanum tuberosum</i> vetispiradiene synthase. PVS4. potato sesquiterpene cyclase.
BAA82092.1	AB022598	<i>Solanum tuberosum</i> vetispiradiene synthase. PVS1. potato sesquiterpene cyclase.
AAF21053.1	AF212433	<i>Capsicum annuum</i> UV-induced sesquiterpene cyclase. SC2.
BAA82109.1	AB022720	<i>Solanum tuberosum</i> vetispiradiene synthase. PVS3. potato sesquiterpene cyclase; PVS3.
BAA82108.1	AB022719	<i>Solanum tuberosum</i> vetispiradiene synthase. PVS2. potato sesquiterpene cyclase; PVS2.
AAC12784.1	U88318	<i>Gossypium hirsutum</i> (E,E)-farnesyl diphosphate cyclizing. (+)-delta-cadinene synthase. cdn1. sesquiterpene cyclase; delta-cadinene synthase.
AAG24640.2	AF304444	<i>Artemisia annua</i> sesquiterpene cyclase.
AAK15641.1	AF326117	<i>Capsicum annuum</i> sesquiterpene cyclase. PSC2.
CAC12731.1	AJ271792	<i>Artemisia annua</i> putative sesquiterpene cyclase. cASC125.
SEQ ID NO: 675		
CAA50609.1	X71609	<i>Nicotiana tabacum</i> ras-related GTP-binding protein.

CAA98166.1	Z73938	Lotus japonicus
GTP-binding protein. RAB5A. rab5A.		
CAC24477.1	AJ296336	Cichorium intybus x Cichorium endivia
GTP binding protein. chi3154.		
CAC24476.1	AJ296335	Cichorium intybus x Cichorium endivia
GTP binding protein. chi3152.		
CAB57220.1	AJ249866	Cichorium intybus x Cichorium endivia
GTP binding protein. gtp2.		
CAB57219.1	AJ249865	Cichorium intybus x Cichorium endivia
GTP binding protein. gtp1.		
CAC24475.1	AJ296334	Cichorium intybus x Cichorium endivia
GTP binding protein. chi3153.		
CAA46112.1	X64941	Nicotiana plumbaginifolia
small GTP binding protein.		
CAC24474.1	AJ296333	Cichorium intybus x Cichorium endivia
GTP binding protein. chi3151.		
CAC19792.1	AJ292320	Oryza sativa
small GTP-binding protein, RAB family. RAB5A protein. rab5A.		
AAD28731.1	AF112964	Triticum aestivum
small GTP-binding protein. Sgp.		
CAA98167.1	Z73939	Lotus japonicus
GTP-binding protein. RAB5B. rab5B.		
CAA06922.1	AJ006225	Mesembryanthemum crystallinum
small GTP-binding protein. rab5B.		
AAG42497.1	AF323991	Oryza sativa
small GTP-binding protein RAB5B. rab5B.		
BAA84717.1	AB032761	Oryza sativa
GTP-binding protein. rab5B.		
AAG24438.1	AF304518	Oryza sativa
small GTP-binding protein RAB5B. rab5B.		
CAB57221.1	AJ249867	Cichorium intybus x Cichorium endivia
GTP binding protein. b1.5.		
CAA98180.1	Z73952	Lotus japonicus
GTP-binding protein. RAB11D. rab11D.		
CAA98181.1	Z73953	Lotus japonicus
GTP-binding protein. RAB11E. rab11E.		
BAA02114.1	D12546	Pisum sativum
GTP-binding protein.		
BAA02113.1	D12545	Pisum sativum
GTP-binding protein.		
BAA02116.1	D12548	Pisum sativum
GTP-binding protein.		

BAA02112.1	D12544	Pisum sativum	GTP-binding protein.
BAA02118.1	D12550	Pisum sativum	GTP-binding protein.
CAA98159.1	Z73931	Lotus japonicus	GTP-binding protein. RAB1B. rab1B.
CAB65172.1	AJ245570	Lycopersicon esculentum	putative role in secretion of cell wall modifying enzymes. Rab11 GTPase. Rab11a.
CAA89049.1	Z49190	Beta vulgaris	GTP-binding. small G protein.
BAA02110.1	D12542	Pisum sativum	GTP-binding protein.
AAB97114.1	U58853	Glycine max	small GTP-binding protein. sra1.
BAA02904.1	D13758	Oryza sativa	ras-related GTP binding protein. ss230.
CAA98178.1	Z73950	Lotus japonicus	GTP-binding protein. RAB11B. rab11B.
CAA98177.1	Z73949	Lotus japonicus	GTP-binding protein. RAB11A. rab11A.
AAK15703.1	AF327517	Oryza sativa	GTP-binding protein.
AAF65510.1	AF108883	Capsicum annuum	small GTP-binding protein.
BAA76422.1	AB024994	Cicer arietinum	rab-type small GTP-binding protein.
CAA98160.1	Z73932	Lotus japonicus	GTP-binding protein. RAB1C. rab1C.
AAA80680.1	U38466	Lycopersicon esculentum	small GTP-binding protein. LeRab1C. ; YPT1/Rab1A homolog LeRab1C.
AAA80678.1	U38464	Lycopersicon esculentum	small GTP-binding protein. LeRab1A. ; YPT1/Rab1A homolog LeRab1A.
SEQ ID NO: 676			
AAA80499.1	U20594	Lycopersicon esculentum	leucine aminopeptidase.
CAA54314.1	X77015	Solanum tuberosum	leucine aminopeptidase. LAP.
CAA48038.1	X67845	Solanum tuberosum	leucine aminopeptidase. LAP.
AAC49457.1	U50152	Lycopersicon esculentum	peptidase. leucine aminopeptidase. lap2.

AAC49456.1	U50151	Lycopersicon esculentum exoprotease in the defense response. leucine aminopeptidase. lap.
AAA80498.1	U20593	Lycopersicon esculentum leucine aminopeptidase.
CAA68143.1	X99825	Petroselinum crispum cytosol aminopeptidase. leucine aminopeptidase.
BAA90521.1	AB037678	Phaseolus vulgaris leucine aminopeptidase.
SEQ ID NO: 678		
CAC09580.1	AJ298992	Fagus sylvatica Absciscic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.
AAA34002.1	M67449	Glycine max protein kinase. PK6.
AAK11734.1	AY027437	Arachis hypogaea serine/threonine/tyrosine kinase.
BAB16918.1	AP002863	Oryza sativa putative protein kinase. P0005A05.22.
CAA06334.1	AJ005077	Lycopersicon esculentum protein kinase. TCTR2 protein. TCTR2.
AAG31141.1	AF305911	Oryza sativa EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
CAA73722.1	Y13273	Lycopersicon esculentum putative protein kinase.
AAD46406.1	AF096250	Lycopersicon esculentum ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.
AAG31142.1	AF305912	Hordeum vulgare EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAD10056.1	AF110518	Lycopersicon esculentum ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.
AAD10057.1	AF110519	Lycopersicon esculentum ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.
AAK30005.1	AY029067	Rosa hybrid cultivar CTR2 protein kinase.
BAB39409.1	AP002901	Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAA87853.1	AP000816	Oryza sativa EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

BAA06538.1	D31737	Nicotiana tabacum	protein-serine/threonine kinase.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAA94528.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).
BAB17126.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.16.
BAB39451.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.24.
BAB17348.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.32.
BAB17321.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.1.
BAB17129.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.20.
AAF68398.1	AF237568	Oryza sativa	receptor-like protein kinase. RLG2.
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
BAA94517.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB17335.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.17. contains ESTs D47575(S13157),AU032665(S13157).
BAB39441.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.11.
BAB17116.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.3.
AAF78044.1	AF248493	Oryza sativa	receptor-like kinase. RLG18. protein kinase.
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
BAB17127.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.17.
AAF78021.1	AF238477	Oryza sativa	receptor-like kinase. RLG5. protein kinase.
AAD46420.1	AF100771	Hordeum vulgare	receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.
AAD46917.1	AF164021	Oryza sativa	receptor kinase.
BAB17345.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.29.

BAB39438.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.7.
AAF78018.1	AF238474	Oryza sativa	receptor-like kinase. RLG16. protein kinase.
AAC01746.1	AF044489	Oryza sativa	receptor-like protein kinase. drpk1.
BAB17337.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.21. contains ESTs D47575(S13157),AU032665(S13157).
BAB17347.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.31. contains ESTs D47575(S13157),AU032665(S13157).
BAB17344.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.28. contains ESTs D47575(S13157),AU032665(S13157).
BAB39437.1	AP003338	Oryza sativa	receptor-like kinase. OJ1212_B09.6.
AAF78019.1	AF238475	Oryza sativa	receptor-like kinase. RLG17. protein kinase.
BAA05648.1	D26601	Nicotiana tabacum	protein kinase.
BAB17332.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.13. contains ESTs D47575(S13157),AU032665(S13157).
BAB39435.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.2.
SEQ ID NO: 679			
CAA78386.1	Z13996	Petunia x hybrida	DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
CAB43399.1	AJ006292	Antirrhinum majus	Myb-related transcription factor mixta-like 1. mybml1.
CAA67600.1	X99210	Lycopersicon esculentum	myb-related transcription factor. THM16.
BAA23337.1	D88617	Oryza sativa	transfactor. OSMYB1. Osmyb1.
AAA82943.1	U39448	Picea mariana	MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the maize C1.
CAA64614.1	X95296	Lycopersicon esculentum	transcription factor. THM27. myb-related.
BAA93038.1	AP001552	Oryza sativa	EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).

AAC04720.1	AF034134	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-O. similar to MYB A encoded by GenBank Accession Number L04497.
CAA72186.1	Y11351	Oryza sativa	myb factor. myb.
AAF22256.1	AF161711	Pimpinella brachycarpa	myb-related transcription factor.
BAB39987.1	AP003020	Oryza sativa	putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
BAB39972.1	AP003018	Oryza sativa	putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).
BAA23338.1	D88618	Oryza sativa	transfactor. OSMYB2. Osmyb2.
BAA88222.1	AB028650	Nicotiana tabacum	myb-related transcription factor LBM2. lbm2.
CAA67575.1	X99134	Lycopersicon esculentum	transcription factor. THM6. myb-related.
CAA78387.1	Z13997	Petunia x hybrida	DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
CAA66952.1	X98308	Lycopersicon esculentum	THM18. myb-related transcription factor.
BAA23339.1	D88619	Oryza sativa	transfactor. OSMYB3. Osmyb3.
AAC49394.1	U57002	Zea mays	P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the C-terminal.
AAB41101.1	U72762	Nicotiana tabacum	transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.
AAA33500.1	M73028	Zea mays	myb-like transcription factor. P.
AAG36774.1	AF210616	Zea mays	P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.
BAA88223.1	AB028651	Nicotiana tabacum	myb-related transcription factor LBM3. lbm3.
BAA88224.1	AB028652	Nicotiana tabacum	myb-related transcription factor LBM4. lbm4.
CAA72187.1	Y11352	Oryza sativa	myb factor. myb.



BAA88221.1	AB028649	Nicotiana tabacum	myb-related transcription factor LBM1. lbm1.
CAA72185.1	Y11350	Oryza sativa	myb factor. myb.
AAG13574.1	AC037425	Oryza sativa	myb factor. OSJNBa0055P24.4.
SEQ ID NO: 680			
AAA34238.1	L20507	Vigna radiata	calmodulin.
AAA34014.1	L01432	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAA34013.1	L01430	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-1. putative.
CAA36644.1	X52398	Medicago sativa	calmodulin (AA 1-149).
AAD10245.1	AF030033	Phaseolus vulgaris	calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
AAD10244.1	AF030032	Phaseolus vulgaris	calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
CAA74307.1	Y13974	Zea mays	calmodulin.
CAA46150.1	X65016	Oryza sativa	calmodulin. cam.
AAC36058.1	AF042839	Oryza sativa	calmodulin. CaM2.
AAD10246.1	AF030034	Phaseolus vulgaris	calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
CAA54583.1	X77397	Zea mays	calmodulin. CaM2.
BAA87825.1	AP000815	Oryza sativa	ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene. Similar to O.sativa gene encoding calmodulin. (Z12828).
AAA92681.1	U13882	Pisum sativum	calcium-binding protein. calmodulin.
AAA33706.1	M80836	Petunia x hybrida	calmodulin. CAM81.
AAA33705.1	M80831	Petunia x hybrida	calmodulin-related protein. CAM53.
CAA43143.1	X60738	Malus x domestica	Calmodulin. CaM.

CAA78301.1	Z12839	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin. putative.
CAA42423.1	X59751	Daucus carota	calmodulin. Ccam-1.
CAA67054.1	X98404	Capsicum annuum	calmodulin-2.
AAG27432.1	AF295637	Elaeis guineensis	calmodulin.
AAG11418.1	AF292108	Prunus avium	calmodulin.
AAA34237.1	L20691	Vigna radiata	calmodulin.
AAC49587.1	U49105	Triticum aestivum	calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	Triticum aestivum	calmodulin TaCaM3-3. calcium-binding protein.
AAC49585.1	U49103	Triticum aestivum	calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum	calmodulin TaCaM3-1. calcium-binding protein.
AAC49583.1	U48692	Triticum aestivum	calmodulin TaCaM2-3. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum	calmodulin TaCaM2-2. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum	calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	Triticum aestivum	calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	Triticum aestivum	calmodulin TaCaM1-1. calcium-binding.
AAA03580.1	L01431	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-2. putative.
AAB36130.1	S81594	Vigna radiata	auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from Fig. 1; arCaM.
AAA33901.1	L18913	Oryza sativa	calcium binding protein, signal transduction. calmodulin. putative.
CAA78287.1	Z12827	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
AAB46588.1	U83402	Capsicum annuum	calmodulin.

CAA61980.1	X89890	Bidens pilosa	Calmodulin.
AAA32938.1	M27303	Hordeum vulgare	calmodulin.
BAA88540.1	AP000969	Oryza sativa	ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene. Similar to calmodulin. (AF042840).
AAF65511.1	AF108889	Capsicum annuum	calmodulin.
AAC36059.1	AF042840	Oryza sativa	calmodulin. CaM1.
AAA33900.1	L18914	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
CAA78288.1	Z12828	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
AAA34015.1	L01433	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-4. putative.
AAA16320.1	L14071	Bryonia dioica	calmodulin. Bc329. calcium-binding sites (amino acid #): 1. (21..33); 2. (57..68); 3. (94..106); 4. (130..141).
AAA19571.1	U10150	Brassica napus	calcium binding. calmodulin. bcm1.
AAA87347.1	M88307	Brassica juncea	calmodulin.
CAA52602.1	X74490	Zea mays	Calmodulin. ZMCALM1.
SEQ ID NO: 683			
CAA71800.1	Y10847	Brassica juncea	O-acetylserine(thiol) lyase.
CAA71798.1	Y10845	Brassica juncea	O-acetylserine(thiol) lyase.
AAC25635.1	AF044172	Solanum tuberosum	cysteine synthase. CS-A; O-acetylserine (thiol) lyase; cytosolic isoform.
BAA01279.1	D10476	Spinacia oleracea	O-acetylserine(thiol) lyase.
BAA02438.1	D13153	Triticum aestivum	O-acetylserine (thiol) lyase. cys1.
CAA59798.1	X85803	Zea mays	O-acetylserine (thiol) lyase. Mcysp. cysteine synthase.
AAD23907.1	AF073695	Oryza sativa	cysteine synthase. rcs1. O-acetylserine(thiol)-lyase.
AAD23909.1	AF073697	Oryza sativa	cysteine synthase. rcs3. O-acetylserine(thiol)-lyase.

AAC25636.1	AF044173	Solanum tuberosum	cysteine synthase. CS-B; O-acetylserine (thiol) lyase; plastidic isoform.
AAC27794.1	AF078693	Chlamydomonas reinhardtii	cysteine biosynthesis. putative O-acetylserine(thiol)lyase precursor. Crcys-1A.
CAA06819.1	AJ006024	Cicer arietinum	cysteine synthase, O-acetyl-L-serine (thiol)-lyase.
CAA46086.1	X64874	Capsicum annuum	O-acetylserine (thiol)-lyase.
CAA71799.1	Y10846	Brassica juncea	O-acetylserine(thiol) lyase.
AAA16973.1	L05184	Chloroplast Spinacia oleracea	O-acetylserine-(thiol)-lyase.
AAD23908.1	AF073696	Oryza sativa	cysteine synthase. rcs2. O-acetylserine(thiol)-lyase.
AAD23910.1	AF073698	Oryza sativa	cysteine synthase. rcs4. O-acetylserine(thiol)-lyase.
SEQ ID NO: 684			
AAA68983.1	L12395	Brassica napus	signal transduction, membrane vehicle traffic. small GTP-binding protein. bra. putative.
SEQ ID NO: 685			
AAB61961.1	L81152	Oryza sativa	integral membrane protein. OsNramp2.
AAB36424.1	S81897	Oryza sativa	OsNramp1. OsNramp1. Nramp1 homolog/Bcg product homolog; This sequence comes from Fig. 2.
AAB62273.1	L41217	Oryza sativa	integral membrane protein. OsNramp1. putative.
AAC49720.1	U60767	Oryza sativa	integral membrane protein OsNramp3. OsNramp3.
SEQ ID NO: 686			
AAC04719.1	AF034133	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-N. similar to MYB A encoded by GenBank Accession Number L04497.
AAB58314.1	U33917	Craterostigma plantagineum	Cpm7. cpm7. putative DNA-binding protein; myb-like gene; myb-related transcription factor.
AAB58313.1	U33916	Craterostigma plantagineum	Cpm5. cpm5. putative DNA-binding protein; myb-related gene; myb-related transcription factor.
AAC13876.1	U33915	Craterostigma plantagineum	myb-related transcription factor Cpm10. cpm10. putative DNA-binding protein.

AAK08983.1	AY026332	Oryza sativa	Myb transcription factor JAMyb. related to host cell death and defense responses; induced by jasmonic acid, wounding, or infection of rice blast fungus, but not by salicylic acid or abscisic acid.
BAB18296.1	AP002860	Oryza sativa	putative myb-related transcription factor. P0409B08.23.
CAA71992.1	Y11105	Pisum sativum	Myb26.
BAB40790.1	AB058642	Lilium hybrid division I	LhMyb.
AAK19618.1	AF336285	Gossypium hirsutum	GHMYB38. ghmyb38. similar to myb.
CAA78387.1	Z13997	Petunia x hybrida	DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
BAA88221.1	AB028649	Nicotiana tabacum	myb-related transcription factor LBM1. lbm1.
BAA88224.1	AB028652	Nicotiana tabacum	myb-related transcription factor LBM4. lbm4.
AAK19617.1	AF336284	Gossypium hirsutum	GHMYB36. ghmyb36. similar to myb.
AAA33067.1	L04497	Gossypium hirsutum	MYB A; putative.
AAK19615.1	AF336282	Gossypium hirsutum	GHMYB10. ghmyb10. similar to myb.
BAA81733.2	AB029162	Glycine max	GmMYB29A2.
BAA81732.1	AB029161	Glycine max	GmMYB29A2.
BAA81730.1	AB029159	Glycine max	GmMYB29A1.
BAA88223.1	AB028651	Nicotiana tabacum	myb-related transcription factor LBM3. lbm3.
AAB41101.1	U72762	Nicotiana tabacum	transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.
BAA81736.1	AB029165	Glycine max	GmMYB29B2.
BAA81731.1	AB029160	Glycine max	GmMYB29A1.
CAA72218.1	Y11415	Oryza sativa	myb.

CAA67000.1	X98355	Oryza sativa	activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.
AAK19611.1	AF336278	Gossypium hirsutum	BNLGH233. bnlghi6233. similar to myb.
CAA67575.1	X99134	Lycopersicon esculentum	transcription factor. THM6. myb-related.
CAA64614.1	X95296	Lycopersicon esculentum	transcription factor. THM27. myb-related.
AAD31395.1	AF114162	Lolium temulentum	gibberellin MYB transcription factor. GAMyb. R2/R3-MYB.
BAA93038.1	AP001552	Oryza sativa	EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).
AAG22863.1	AY008692	Hordeum vulgare	transcription factor GAMyb. Gamyb.
BAA96421.1	AB044084	Triticum aestivum	transcription activator for gibberellin response. GAMyb protein. Ta-GAMyb.
CAA61021.1	X87690	Hordeum vulgare	transcriptional activator of alpha-amylase gene promoter. GAMyb protein. Gam1.
CAA66952.1	X98308	Lycopersicon esculentum	THM18. myb-related transcription factor.
AAC49394.1	U57002	Zea mays	P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the C-terminal.
BAA88222.1	AB028650	Nicotiana tabacum	myb-related transcription factor LBM2. lbm2.
AAG36774.1	AF210616	Zea mays	P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.
AAA33500.1	M73028	Zea mays	myb-like transcription factor. P.
CAC19439.1	AJ237661	Oryza sativa	Myb factor protein. myb.
CAB40189.1	AJ133638	Avena sativa	transcriptional activator. myb protein. gamyb.
AAK19619.1	AF336286	Gossypium hirsutum	GHMYB9. ghmyb9. similar to myb.
AAC04720.1	AF034134	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-O. similar to MYB A encoded by GenBank Accession Number L04497.
AAC04716.1	AF034130	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-D. similar to MYB A encoded by GenBank Accession Number L04497.

AAG28526.1	AF198499	Nicotiana tabacum	anther-specific myb-related protein 1. mybAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.
CAA78388.1	Z13998	Petunia x hybrida	DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb proto-oncoproteins.
AAA33482.1	M37153	Zea mays	c1 locus myb homologue; putative.
AAK09327.1	AF320614	Zea mays	activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.
AAK09326.1	AF320613	Zea mays	activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.
SEQ ID NO: 687			
BAA92972.1	AP001551	Oryza sativa	ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).
BAA83689.1	AB011968	Oryza sativa	OsPK7. OsPK7. protein kinase.
BAA83688.1	AB011967	Oryza sativa	OsPK4. OsPK4. protein kinase.
AAF22219.1	AF141378	Zea mays	protein kinase PK4. ZmPK4.
BAA34675.1	AB011670	Triticum aestivum	wpk4 protein kinase. wpk4.
CAA73068.1	Y12465	Sorghum bicolor	serine/threonine kinase. SNFL2.
CAA73067.1	Y12464	Sorghum bicolor	serine/threonine kinase. SNFL1.
BAA92970.1	AP001551	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4 BAC clone F28A21 ; putative protein kinase. (AL035526).
CAA74646.1	Y14274	Sorghum bicolor	putative serine/threonine protein kinase. SNFL3.
AAD31900.1	AF145482	Mesembryanthemum crystallinum	putative serine/threonine protein kinase.
AAB62693.1	AF004947	Oryza sativa	protein kinase.
BAA96628.1	AP002482	Oryza sativa	ESTs D41739(S4522),AU055999(S20214), AU057588(S21592) correspond to a region of the predicted gene. Similar to Sorghum bicolor serine/threonine kinase (Y12465).

AAD23582.1	AF128443	Glycine max	probably involved in plant stress responses possibly regulates gene expression. SNF-1-like serine/threonine protein kinase. expressed in nodules, roots and leaves.
BAA05649.1	D26602	Nicotiana tabacum	protein kinase.
CAA71142.1	Y10036	Cucumis sativus	SNF1-related protein kinase.
AAC99329.1	AF062479	Oryza sativa	protein kinase SNF1. Snf1. similar to yeast SNF1.
CAA65244.1	X95997	Solanum tuberosum	SNF1-related protein kinase. PKIN1.
CAA57898.1	X82548	Hordeum vulgare	SNF1-related protein kinase. BKIN2.
CAA07813.1	AJ007990	Hordeum vulgare	SnRK1-type protein kinase. kin12a.
CAA46556.1	X65606	Hordeum vulgare	protein kinase. BKIN12.
AAB05457.1	U55768	Oryza sativa	SNF1-related protein kinase. RSk1. Ser/Thr protein kinase homolog.
CAA46554.1	X65604	Hordeum vulgare	protein kinase. BKIN12.
AAD00239.1	U73938	Nicotiana tabacum	protein kinase. PK11-C1. PK11-C1. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.
AAC69450.1	AF032465	Nicotiana tabacum	putative serine/threonine protein kinase. WAPK.
AAD00240.1	U73939	Nicotiana tabacum	protein kinase. PK11-C5. PK11-C5. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.
BAA13608.1	D88399	Oryza sativa	serine-threonine kinase. endosperm kinase. REK.
AAA34017.1	L19360	Glycine max	protein kinase 2. SPK-2. putative.
AAG60195.1	AC084763	Oryza sativa	protein kinase REK. OSJNBa0027P10.6.
AAA33004.1	L12394	Brassica napus	serine/threonine protein kination. serine/threonine protein kinase. BSK2. putative.
BAA19573.1	AB002109	Oryza sativa	protein kinase. a novel protein kinase.
AAA33979.1	L01453	Glycine max	protein phosphorylation, regulatory protein. protein kinase. SPK-1. putative.
AAA33003.1	L12393	Brassica napus	protein kination. serine/threonine protein kinase. BSK1. putative.



AAB68962.1	L38855	Glycine max protein kinase. SPK-4.
AAB68961.1	L19361	Glycine max protein kinase 3. SPK-3. putative.
AAB58348.1	U29095	Triticum aestivum serine-threonine protein kinase. TaPK3.
AAF27340.1	AF186020	Vicia faba abscisic acid-activated protein kinase. AAPK.
AAA96325.1	M94726	Triticum aestivum protein kinase. abscisic acid inducible.
CAA81443.1	Z26846	Mesembryanthemum crystallinum protein kinase. MCPK9.
AAG31326.1	AF178575	Vitis vinifera putative serine/threonine kinase GDBrPK. GDBrPK. similar to SNF protein kinase.
CAA06503.1	AJ005373	Craterostigma plantagineum protein kinase. cppk1.
AAF21062.1	AF216527	Dunaliella tertiolecta calcium-dependent protein kinase. CPK1; CDPK.
CAA89202.1	Z49233	Chlamydomonas eugametos calcium-stimulated protein kinase.
SEQ ID NO: 689		
AAC49826.1	U71604	Catharanthus roseus involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4- hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.
AAB97311.1	AF008597	Catharanthus roseus desacetoxyvindoline-4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase; involved in the second to last step in vindoline biosynthesis.
AAC49827.1	U71605	Catharanthus roseus involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4- hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.
BAA37127.1	AB012203	Lactuca sativa 2-oxoglutarate-dependent dioxygenase. gibberelin 20-oxidase. Ls20ox1.
BAA95828.1	AP002069	Oryza sativa ESTs D47168(S12332),D46350(S10967) correspond to a region of the predicted gene. Similar to Prunus armeniaca ethylene-forming-enzyme-like dioxygenase. (U97530).
AAD56580.1	AF184273	Daucus carota leucoanthocyanidin dioxygenase 1. LDOX1. 2-oxoglutarate dependent dioxygenase.
AAB39995.1	U82432	Dianthus caryophyllus anthocyanidin synthase. allele: S; 2-oxoglutarat-dependent dioxygenase.
AAD56581.1	AF184274	Daucus carota leucoanthocyanidin dioxygenase 2. LDOX. 2-oxoglutarate dependent dioxygenase.
SEQ ID NO: 691		

AAA34002.1	M67449	Glycine max	protein kinase. PK6.
CAC09580.1	AJ298992	Fagus sylvatica	Abscisic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.
AAK11734.1	AY027437	Arachis hypogaea	serine/threonine/tyrosine kinase.
BAB16918.1	AP002863	Oryza sativa	putative protein kinase. P0005A05.22.
CAA06334.1	AJ005077	Lycopersicon esculentum	protein kinase. TCTR2 protein. TCTR2.
AAD10057.1	AF110519	Lycopersicon esculentum	ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.
AAD10056.1	AF110518	Lycopersicon esculentum	ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.
CAA73722.1	Y13273	Lycopersicon esculentum	putative protein kinase.
AAD46406.1	AF096250	Lycopersicon esculentum	ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.
AAG31141.1	AF305911	Oryza sativa	EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAG31142.1	AF305912	Hordeum vulgare	EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAK30005.1	AY029067	Rosa hybrid cultivar	CTR2 protein kinase.
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
AAF91324.1	AF244890	Glycine max	receptor-like protein kinase 3. RLK3. GmRLK3.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.

BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAK16409.1	AF320086	Zea mays	serine threonine kinase 1. stk1. expressed in mature tassel.
BAA06538.1	D31737	Nicotiana tabacum	protein-serine/threonine kinase.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
CAB54520.1	AJ238845	Brassica napus	putative role in cell cycle control. MAP3K epsilon 1 protein kinase. MAP3Ke1.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
CAA08995.1	AJ010091	Brassica napus	MAP3K alpha 1 protein kinase. MAP3K alpha 1.
BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
BAB40021.1	AP003021	Oryza sativa	putative wall-associated kinase 2. P0503E05.25. contains EST C24950(S16264).
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
BAB40010.1	AP003021	Oryza sativa	putative wall-associated kinase 2. P0503E05.12.
AAC36318.1	AF053127	Malus x domestica	leucine-rich receptor-like protein kinase. LRPKm1.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
BAB18321.1	AP002865	Oryza sativa	putative receptor protein kinase. P0034C11.11.

BAA92836.1 AB032473 Brassica oleracea  
S18 S-locus receptor kinase. SRK18.

AAA33915.1 L27821 Oryza sativa  
receptor type serine/threonine kinase. protein kinase.

BAB40081.1 AP003074 Oryza sativa  
putative receptor protein kinase. OSJNBa0004G10.30.

AAD38286.1 AC007789 Oryza sativa  
putative protein kinase. OSJNBa0049B20.13.

BAA92837.1 AB032474 Brassica oleracea  
S60 S-locus receptor kinase. SRK60.

SEQ ID NO: 692

AAK16172.1 AC079887 Oryza sativa  
putative glucosyltransferase. OSJNBa0040E01.14.

AAF17077.1 AF199453 Sorghum bicolor  
UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.

AAF61647.1 AF190634 Nicotiana tabacum  
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAA89009.1 AB027455 Petunia x hybrida  
anthocyanin 5-O-glucosyltransferase. PH1.

AAF98390.1 AF287143 Brassica napus  
catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

AAD21086.1 AF127218 Forsythia x intermedia  
adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.

BAA93039.1 AB033758 Citrus unshiu  
limonoid UDP-glucosyltransferase. LGTase.

BAA83484.1 AB031274 Scutellaria baicalensis  
UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

BAA12737.1 D85186 Gentiana triflora  
UDP-glucose:flavonoid-3-glucosyltransferase.

CAA54612.1 X77462 Manihot esculenta  
UTP-glucose glucosyltransferase. CGT5.

BAA19155.1 AB000623 Nicotiana tabacum  
glucosyl transferase. JIGT.

BAA89008.1 AB027454 Petunia x hybrida  
anthocyanidin 3-O-glucosyltransferase. PGT8.

BAB17060.1 AP002523 Oryza sativa  
putative glucosyl transferase. P0013F10.6.

BAA90787.1 AB038248 Ipomoea batatas  
UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.

AAK16178.1	AC079887	<i>Oryza sativa</i> putative glucosyltransferase. OSJNBa0040E01.5.
AAK16175.1	AC079887	<i>Oryza sativa</i> putative glucosyltransferase. OSJNBa0040E01.15.
AAB36653.1	U32644	<i>Nicotiana tabacum</i> immediate-early salicylate-induced glucosyltransferase. IS5a.
AAB36652.1	U32643	<i>Nicotiana tabacum</i> immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28303.1	AF346431	<i>Nicotiana tabacum</i> phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
AAK28304.1	AF346432	<i>Nicotiana tabacum</i> phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
BAB17061.1	AP002523	<i>Oryza sativa</i> putative glucosyl transferase. P0013F10.7. contains EST C73149(E2992).
CAA30761.1	X07940	<i>Zea mays</i> UDPglucose flavonoid glycosyl-transferase. Bz-McC.
AAK16410.1	AF320086	<i>Zea mays</i> UDPG-flavonoid 3-O-glucosyl transferase. bz.
CAA31855.1	X13500	<i>Zea mays</i> UDPglucose:flavonol 3-O-glucosyltransferase.
BAB17059.1	AP002523	<i>Oryza sativa</i> putative glucosyl transferase. P0013F10.5.
BAA36421.1	AB013596	<i>Perilla frutescens</i> UDP-glucose:anthocynsin 5-O-glucosyltransferase. PF3R4.
AAB86473.1	AF028237	<i>Ipomoea purpurea</i> UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.
CAA30760.1	X07937	<i>Zea mays</i> UDPglucose flavonoid glycosyl transferase. Bz-W22.
BAB41021.1	AB047094	<i>Vitis vinifera</i> UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAB41019.1	AB047092	<i>Vitis vinifera</i> UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAB41025.1	AB047098	<i>Vitis vinifera</i> UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
AAD55985.1	AF165148	<i>Petunia x hybrida</i> catalyzes the penultimate step of flavonol glucosylgalactoside biosynthesis from UDP-galactose and flavonol aglycones in petunia pollen. UDP-galactose:flavonol 3-O-galactosyltransferase. F3galtase.
BAB41018.1	AB047091	<i>Vitis labrusca x Vitis vinifera</i> UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents <i>V. vinifera</i> cv. Centennial.

BAB41017.1	AB047090	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
AAK16181.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.16.
BAB41023.1	AB047096	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
CAA59450.1	X85138	Lycopersicon esculentum	twil. homologous to glucosyltransferases.
CAA54614.1	X77464	Manihot esculenta	UTP-glucose glucosyltransferase. CGT7.
AAB81682.1	AF000371	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
AAB81683.1	AF000372	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41024.1	AB047097	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
CAA54558.1	X77369	Solanum melongena	glycosyl transferase. GT.
BAB41026.1	AB047099	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
BAB41020.1	AB047093	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
BAB41022.1	AB047095	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAA19659.1	AB002818	Perilla frutescens	flavonoid 3-O-glucosyltransferase. UDP glucose.
AAG25643.1	AF303396	Phaseolus vulgaris	UDP-glucosyltransferase HRA25. putative; defense associated.
SEQ ID NO: 694			
BAB40923.1	AB059401	Oryza sativa	putative selenium binding protein. Os SBP.
SEQ ID NO: 695			
AAD26942.1	AF119050	Datisca glomerata	zinc-finger protein 1. zfp1. DgZFP1.
BAA05079.1	D26086	Petunia x hybrida	zinc-finger protein.
AAB39638.1	U68763	Glycine max	putative transcription factor. SCOF-1. scof-1. zinc-finger protein.
CAB77055.1	Y18788	Medicago sativa	putative TFIIIA (or kruppel)-like zinc finger protein.
AAC06243.1	AF053077	Nicotiana tabacum	transcription factor. osmotic stress-induced zinc-finger protein. zfp.

BAA05077.1	D26084	Petunia x hybrida	zinc-finger DNA binding protein.
BAA05076.1	D26083	Petunia x hybrida	zinc-finger DNA binding protein.
AAB53260.1	U76554	Brassica rapa	transcription factor. zinc-finger protein-1. BR42.
BAA05078.1	D26085	Petunia x hybrida	zinc-finger DNA binding protein.
AAB53261.1	U76555	Brassica rapa	zinc-finger protein BcZFP1. BcZFP1(3-2z).
AAK01713.1	AF332876	Oryza sativa	zinc finger transcription factor ZF1.
BAA21920.1	AB006598	Petunia x hybrida	ZPT2-11. C2H2 zinc finger protein, 2finger.
BAA21922.1	AB006600	Petunia x hybrida	ZPT2-13. C2H2 zinc finger protein, 2finger.
BAA19112.1	AB000453	Petunia x hybrida	PETHy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.
BAA21927.1	AB006605	Petunia x hybrida	ZPT3-3. C2H2 zinc finger protein, 3 finger.
BAA96071.1	AB035133	Petunia x hybrida	C2H2 zinc-finger protein ZPT3-3. ZPT3-3.
BAA96070.1	AB035132	Petunia x hybrida	C2H2 zinc-finger protein ZPT2-10. PETHy;ZPT2-10.
BAA21919.1	AB006597	Petunia x hybrida	ZPT2-10. C2H2 zinc finger protein, 2 finger.
BAA19114.1	AB000455	Petunia x hybrida	PETHy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.
BAA21921.1	AB006599	Petunia x hybrida	ZPT2-12. C2H2 zinc finger protein, 2 finger.
BAA21928.1	AB006606	Petunia x hybrida	ZPT4-4. C2H2 zinc finger protein, 4 finger.
CAA60828.1	X87374	Pisum sativum	putative zinc finger protein.
BAA21925.1	AB006603	Petunia x hybrida	ZPT2-8. C2H2 zinc finger protein, 2 finger.
BAA19111.1	AB000452	Petunia x hybrida	PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.
BAA19926.1	AB000456	Petunia x hybrida	PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.
BAA21924.1	AB006602	Petunia x hybrida	ZPT2-7. C2H2 zinc finger protein, 2finger.

BAA21923.1	AB006601	Petunia x hybrida
ZPT2-14. C2H2 zinc finger protein, 2 finger.		
BAA21926.1	AB006604	Petunia x hybrida
ZPT2-9. C2H2 zinc finger protein, 2 finger.		
BAA19110.1	AB000451	Petunia x hybrida
PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.		
BAA19113.1	AB000454	Petunia x hybrida
PETHy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.		
SEQ ID NO: 702		
AAK29419.1	AF348319	Zea mays
TERMINAL EAR1. te1. RNA-binding protein; 3 putative RRM motifs; similar to Schizosaccharomyces pombe Mei2 and Arabidopsis AML1; te1 cDNA sequence is presented in GenBank Accession Number AF047852.		
CAA57551.1	X82030	Phaseolus vulgaris
chloroplast RNA binding protein. RNP1.		
CAA66479.1	X97905	Vicia faba
RNA- or ssDNA-binding protein.		
CAC01237.1	AJ292767	Nicotiana plumbaginifolia
nuclear RNA binding protein. RNA Binding Protein 45. rbp45.		
AAF66823.1	AF190655	Nicotiana tabacum
poly(A)-binding protein. PABP.		
AAK30205.1	AF349964	Daucus carota
poly(A)-binding protein. Translin1P.		
AAG59664.1	AC084319	Oryza sativa
putative RNA binding protein. OSJNBa0004B24.1.		
AAB38974.1	U81318	Triticum aestivum
poly(A)-binding protein. wheatpab.		
CAA81127.1	Z26042	Anemia phyllitidis
Binding to the poly(A)-tail of eukaryotic mRNAs. poly(A)-mRNA binding protein.		
AAA79045.1	U34742	Spinacia oleracea
24 kDa RNA binding protein.		
AAC39368.1	AF043297	Chlamydomonas reinhardtii
poly(A) binding protein RB47. PABP.		
AAF63202.1	AF240679	Cucumis sativus
poly(A)-binding protein.		
CAA11894.1	AJ224325	Hordeum vulgare
nucleic acid-binding protein. cp33Hv.		
AAF66825.1	AF190657	Nicotiana tabacum
poly(A)-binding protein. PABP.		
CAA06469.1	AJ005286	Hordeum vulgare
nucleic acid-binding protein. cp31AHv protein.		
SEQ ID NO: 709		



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AAB36546.1 U77940 *Phaseolus vulgaris*  
polyubiquitin. expression is regulated by heavy metal stress, UV, virus infection, heat shock and wounding treatment, this suggests that ubiquitin plays a role in plant defense.

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SEQ ID NO: 714

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CAA61946.1 X89828 *Pisum sativum*  
fructose-1,6-bisphosphate aldolase.

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AAB61592.1 AF003124 *Mesembryanthemum crystallinum*  
fructose-biphosphate aldolase.

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CAB77243.2 AJ133146 *Persea americana*  
glycolytic enzyme, sixth step in glycolysis. fructose-bisphosphate aldolase. alf.

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BAA08845.1 D50307 *Oryza sativa*  
aldolase C-1.

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BAA08830.1 D50301 *Oryza sativa*  
aldolase C-1.

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CAA46649.1 X65742 *Spinacia oleracea*  
fructose-bisphosphate aldolase.

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BAA02729.1 D13512 *Oryza sativa*  
cytoplasmic aldolase.

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AAG21429.1 AF308587 *Fragaria x ananassa*  
cytosolic aldolase. SCA1.

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CAA37290.1 X53130 *Oryza sativa*  
fructose-diphosphate aldolase (AA 1-358).

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CAA31366.1 X12872 *Zea mays*  
fructose bisphosphate aldolase.

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AAA33435.1 M16220 *Zea mays*  
aldolase.

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CAA61947.1 X89829 *Pisum sativum*  
fructose-1,6-bisphosphate aldolase.

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CAA06308.1 AJ005041 *Cicer arietinum*  
cytosolic fructose-1,6-bisphosphate aldolase.

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AAK19324.1 AF329673 *Dunaliella salina*  
fructose-bisphosphate aldolase isoenzyme 1. salt-induced.

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CAA71408.1 Y10380 *Solanum tuberosum*  
homologous to plastidic aldolases.

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BAA77603.1 AB027002 *Nicotiana paniculata*  
plastidic aldolase.

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BAA77604.1 AB027001 *Nicotiana paniculata*  
plastidic aldolase NPALDP1. NpAldP1.

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AAA33642.1 M97476 *Pisum sativum*  
aldolase.

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AAA33643.1 M97477 *Pisum sativum*  
aldolase.

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BAA02730.1	D13513	Oryza sativa	chloroplastic aldolase.
AAF74220.1	AF216582	Avena sativa	fructose 1,6-bisphosphate aldolase precursor.
CAA47293.1	X66814	Spinacia oleracea	fructose-bisphosphate aldolase.
AAK19325.1	AF329674	Dunaliella salina	fructose-bisphosphate aldolase isoenzyme 2. salt-induced.
CAB46520.1	AJ243524	Phleum pratense	sixth step in glycolysis. putative fructose-bisphosphate aldolase.
CAA09669.1	AJ011516	Scherffelia dubia	fructose-bisphosphate aldolase.
CAA49590.1	X69969	Chlamydomonas reinhardtii	fructose-bisphosphate aldolase. ALDCHL.
AAC60574.1	S72951	Chloroplast Chlamydomonas reinhardtii	fructosediphosphate aldolase. fructosediphosphate aldolase. This sequence comes from Fig. 4.
AAB70542.1	AF017362	Oryza sativa	aldolase.
BAA76430.1	AB025002	Cicer arietinum	fructose-bisphosphate aldolase.
AAD20818.1	AF107590	Dendrobium grex Madame Thong-In	putative fructose-bisphosphate aldolase. otg11.
BAA11395.1	D78500	Brassica rapa	putative aldolase. Sequence homologous to cytoplasmic aldolase of rice (D13512).
BAA78593.1	AU066535	Chlamydomonas sp. HS-5	fructose-bisphosphate aldolase precursor. NaCl inducible.
CAC34412.1	Y18576	Flaveria trinervia	fructose-bisphosphate aldolase. alf.
SEQ ID NO: 715			
AAK07429.1	AF321287	Musa acuminata	beta-glucosidase.
AAC69619.1	AF072736	Pinus contorta	beta-glucosidase.
AAF04007.1	AF163097	Dalbergia cochinchinensis	beta-fucosidase beta-glucosidase. dalcochinin 8'-O-beta-glucoside beta-glucosidase precursor. BGLU1. rotenoid beta-glucosidase.
AAA93032.1	U50201	Prunus serotina	hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase precursor. located in protein bodies of Prunus seeds; encodes 8 putative N-glycosylation sites (N-X-S/T); encodes NEP and ITENG motifs characteristic of the BGA family of beta-glucosidases.
BAA78708.1	AB003089	Polygonum tinctorium	beta-glucosidase.

AAA91166.1	U39228	Prunus avium	beta-glucosidase.
BAA11831.1	D83177	Costus speciosus	saponin metabolite. furostanol glycoside 26-O-beta-glucosidase (F26G). functional expression in <i>E. coli</i> ; one of the F26G isozymes.
AAF34650.1	AF221526	Prunus serotina	hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase isoform PHA precursor. beta-glucosidase; contains 6 potential N-glycosylation sites (N-X-S/T); glycosyl hydrolase family 1 member.
AAG25897.1	AF170087	Cucurbita pepo	silverleaf whitefly-induced protein 3. SLW3. similar to beta-glucosidase.
AAG00614.1	AF293849	Secale cereale	beta-glucosidase.
AAB22162.1	S35175	Manihot esculenta	linamarase. linamarase. beta-glucosidase; Method: conceptual translation with partial peptide sequencing; This sequence comes from Fig. 4.
AAF03675.1	AF149311	Rauvolfia serpentina	hydrolyses the glucoalkaloid raucaffricine. raucaffricine-O-beta-D-glucosidase. beta glucosidase; RG; part of the Ajmaline biosynthesis pathway; belongs to family 1 of the glycosyl hydrolases.
AAA87339.1	L41869	Hordeum vulgare	beta-glucosidase. BGQ60. expression specific to starchy endosperm of seed.
AAC49177.1	U33817	Sorghum bicolor	beta-glucosidase, catalyzes the hydrolysis of the cyanogenic beta-glucoside dhurrin. dhurrinase.
CAA64442.1	X94986	Manihot esculenta	beta glucosidase. bglA.
AAD02839.1	AF082991	Avena sativa	beta-D-glucosidase beta subunit precursor. P60b. avenacosidase.
AAD09850.1	U44087	Zea mays	beta-D-glucosidase precursor. glu2. product subunit structure: autodimer of 58.4 kDa monomers Allele: glu2-B73.
AAD10503.1	U33816	Zea mays	functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
AAB03266.1	U44773	Zea mays	beta-D-glucosidase. glu1. autodimer of 58.4 kD monomers.
AAA65946.1	U25157	Zea mays	functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
CAA52293.1	X74217	Zea mays	beta-glucosidase. p60.1.

AA28800.1	AF112888	<i>Catharanthus roseus</i> plays a role in secondary metabolism by hydrolyzing strictosidine to cathenamine during indole alkaloid biosynthesis. strictosidine beta-glucosidase. localized in the endoplasmic reticulum.
CAA40057.1	X56733	<i>Trifolium repens</i> beta-glucosidase. Li.
CAA40058.1	X56734	<i>Trifolium repens</i> beta-glucosidase. non-cyanogenic.
CAA55196.1	X78433	<i>Avena sativa</i> beta-D-glucosidase.
CAA79989.2	Z21977	<i>Brassica napus</i> beta thioglucosidase. myrosinase, thioglucoside glucohydrolase. Myr1.Bn1.
AAB71381.1	U95298	<i>Manihot esculenta</i> linamarase. pLIN-GEN. beta-glucosidase.
CAA57913.1	X82577	<i>Brassica napus</i> beta-glucosidase. bgl.
AAB38784.1	U72154	<i>Brassica nigra</i> beta-glucosidase. psr3.1. PSR3.1; phosphate-starvation responsive enzyme.
AA24651.1	AF221527	<i>Prunus serotina</i> putative prunasin hydrolase precursor. beta-glucosidase; glycosyl hydrolase family 1 member.
AAA84906.1	U28047	<i>Oryza sativa</i> catalyzes the release of either gibberellin or cyanogenic substances from their glucoconjugates. beta glucosidase. beta-D-glucoside glucohydrolase; dimer of 60 kDa monomers; localized in the plastid.
CAC08209.1	AJ005950	<i>Cicer arietinum</i> beta-glucosidase.
SEQ ID NO: 718		
AA61647.1	AF190634	<i>Nicotiana tabacum</i> UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAA89009.1	AB027455	<i>Petunia x hybrida</i> anthocyanin 5-O-glucosyltransferase. PH1.
BAA93039.1	AB033758	<i>Citrus unshiu</i> limonoid UDP-glucosyltransferase. LGTase.
BAA36423.1	AB013598	<i>Verbena x hybrida</i> UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
BAA36421.1	AB013596	<i>Perilla frutescens</i> UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.
AA98390.1	AF287143	<i>Brassica napus</i> catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
BAA36422.1	AB013597	<i>Perilla frutescens</i> UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.

BAB07962.1	AP002524	<i>Oryza sativa</i>	putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
AAD21086.1	AF127218	<i>Forsythia x intermedia</i>	adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
AAK16178.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.5.
BAA12737.1	D85186	<i>Gentiana triflora</i>	UDP-glucose:flavonoid-3-glucosyltransferase.
AAK16181.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.16.
AAK16175.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.15.
AAK16172.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.14.
CAA59450.1	X85138	<i>Lycopersicon esculentum</i>	twil. homologous to glucosyltransferases.
AAF17077.1	AF199453	<i>Sorghum bicolor</i>	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
BAA89008.1	AB027454	<i>Petunia x hybrida</i>	anthocyanidin 3-O-glucosyltransferase. PGT8.
AAB81683.1	AF000372	<i>Vitis vinifera</i>	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41017.1	AB047090	<i>Vitis labrusca x Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
AAB81682.1	AF000371	<i>Vitis vinifera</i>	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41022.1	AB047095	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41020.1	AB047093	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
BAB41021.1	AB047094	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAB41019.1	AB047092	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAA83484.1	AB031274	<i>Scutellaria baicalensis</i>	UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
BAB41025.1	AB047098	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

BAB41023.1	AB047096	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
BAA90787.1	AB038248	Ipomoea batatas	UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.
BAA19659.1	AB002818	Perilla frutescens	flavonoid 3-O-glucosyltransferase. UDP glucose.
BAB41018.1	AB047091	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.
AAB36652.1	U32643	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
BAB41024.1	AB047097	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
BAB41026.1	AB047099	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
CAA31855.1	X13500	Zea mays	UDPglucose:flavonol 3-O-glucosyltransferase.
AAB86473.1	AF028237	Ipomoea purpurea	UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.
CAA54614.1	X77464	Manihot esculenta	UTP-glucose glucosyltransferase. CGT7.
SEQ ID NO: 719			
AAC24195.1	AF020425	Nicotiana tabacum	calmodulin binding protein. glutamate decarboxylase isozyme 1. NtGAD1. calcium-calmodulin-dependent enzyme.
AAK18620.1	AF352732	Nicotiana tabacum	converts glutamate to gamma-aminobutyric acid. glutamate decarboxylase isozyme 3. GAD; GAD3; NtGAD3; calcium/calmodulin-dependent enzyme.
AAB40608.1	U54774	Nicotiana tabacum	glutamate decarboxylase. NtGAD1. calmodulin regulated enzyme; calmodulin-binding protein.
AAA33710.1	L16977	Petunia x hybrida	glutamate decarboxylase. gad.
AAA33709.1	L16797	Petunia x hybrida	glutamate decarboxylase. gad.
AAC39483.1	AF020424	Nicotiana tabacum	glutamate decarboxylase isozyme 2. NtGAD2. calcium-calmodulin-dependent enzyme.
BAB32870.1	AB056062	Oryza sativa	glutamate decarboxylase. GAD.
BAB32868.1	AB056060	Oryza sativa	glutamate decarboxylase. GAD.

CAA56812.1	X80840	<i>Lycopersicon esculentum</i>	homology to pyroxidal-5'-phosphate-dependant glutamate decarboxylases; putative start codon.
BAB32871.1	AB056063	<i>Oryza sativa</i>	glutamate decarboxylase. GAD.
BAB32869.1	AB056061	<i>Oryza sativa</i>	glutamate decarboxylase. GAD.
CAA50719.1	X71900	<i>Lycopersicon esculentum</i>	histidine decarboxylase. hdc. pyridoxal 5'-phosphate dependant.
SEQ ID NO: 720			
BAA92713.1	AP001389	<i>Oryza sativa</i>	ESTs AU033035(S1515),D39871(S1515) correspond to a region of the predicted gene. Similar to <i>Arabidopsis thaliana</i> chromosome II BAC F22D22 genomic sequence; putative glucan synthase (AC006223).
AAD25952.1	AF085717	<i>Gossypium hirsutum</i>	putative callose synthase catalytic subunit. CFL1. cotton FKS1-like protein; similar to <i>Saccharomyces cerevisiae</i> beta-1,3-glucan synthase subunit FKS1.
SEQ ID NO: 721			
CAB55396.1	AL117264	<i>Oryza sativa</i>	zwh12.1. similar to <i>Arabidopsis</i> putative UDP-galactase-4-epimerase (AC007060); Method: conceptual translation with partial peptide sequencing.
CAA06339.1	AJ005082	<i>Cyamopsis tetragonoloba</i>	UDP-galactose 4-epimerase.
AAA86532.1	U31544	<i>Pisum sativum</i>	catabolism of galactose to glucose in Leloir pathway, and in galactose synthesis from glucose. UDP-galactose-4-epimerase. galE. galactowaldenase.
CAA06338.1	AJ005081	<i>Cyamopsis tetragonoloba</i>	UDP-galactose 4-epimerase.
BAB40967.1	AB059568	<i>Pisum sativum</i>	biosynthesis of UDP-D-xylose. UDP-D-glucuronate carboxy-lyase. uxs1.
SEQ ID NO: 726			
BAA88198.1	AP000837	<i>Oryza sativa</i>	Similar to human dimethylaniline monooxygenase (AC002376).
BAA35120.1	AB008845	<i>Oryza sativa</i>	NADH dependent Glutamate Synthase.
AAB41904.1	L37606	<i>Medicago sativa</i>	NADH-dependent glutamate synthase.
BAA88195.1	AP000837	<i>Oryza sativa</i>	Similar to human dimethylaniline monooxygenase (AC002376).

AAB46617.1 L01660 *Medicago sativa*  
the 3 cysteine residues in this region (amino acid residues 1246-1257) may serve to coordinate the [3Fe-4S] cluster that is probably found in this protein. See Knaff et al. (1991) J. Biol. Chem.266:150. NADH-glutamate synthase. NADH-GOGAT; activity increases dramatically during nodule development; the 3 cysteine residues in this region may serve to coordinate the [3Fe-4S] cluster that is probably found in this protein. See Knaff et al. (1991) J. Biol. Chem.266:15080-15084.

## SEQ ID NO: 728

AAG43550.1 AF211532 *Nicotiana tabacum*  
Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.

BAA96875.1 AB045121 *Oryza sativa*  
RING finger 1. RRF1.

AAK00436.1 AC060755 *Oryza sativa*  
putative zinc finger protein. OSJNBa0003O19.23.

BAA78746.1 AB023482 *Oryza sativa*  
Similar to Arabidopsis thaliana RING-H2 finger protein RHX1a mRNA, partial cds.(AF079184).

CAA74911.1 Y14573 *Hordeum vulgare*  
ring finger protein. putative.

AAG46117.1 AC073166 *Oryza sativa*  
putative ring finger protein. OSJNBb0064P21.7.

BAA85438.1 AP000616 *Oryza sativa*  
similar to RING-H2 finger protein RHA1a (AF078683).

BAA77204.1 AB026262 *Cicer arietinum*  
ring finger protein.

## SEQ ID NO: 730

AAA86424.1 U44386 *Lycopersicon esculentum*  
heat shock protein. TFHS1. similar to protein encoded by the arg2 gene in mung bean, encoded by Genbank Accession Number D14411.

## SEQ ID NO: 731

CAA06756.1 AJ005899 *Nicotiana tabacum*  
G subunit. G subunit of Vacuolar-type H<sup>+</sup>-ATPase. vag1.

CAA06757.1 AJ005900 *Nicotiana tabacum*  
Subunit G of vacuolar-type H<sup>+</sup>-ATPase. vag2. vag2.

AAD56039.1 AF184068 *Citrus limon*  
vacuolar membrane ATPase subunit G. LVMA10. V-ATPase VMA10.

## SEQ ID NO: 737

AAF69008.1 AF257779 *Oryza sativa*  
stress-inducible protein. OsSII.

## SEQ ID NO: 739

CAC12996.1 AJ299398 *Medicago truncatula*  
putative auxin import. putative AUX1-like permease. lax2.



AAF21982.1	AF115543	Populus tremula x Populus tremuloides AUX1-like protein. PAX1.
AAG17171.1	AF190880	Populus tremula x Populus tremuloides putative AUX1-like permease. pax5.
CAC12995.1	AJ299397	Medicago truncatula putative auxin import. putative AUX1-like permease. lax1.
CAC12997.1	AJ299399	Medicago truncatula putative auxin import. putative AUX1-like permease. lax3.
CAB65535.1	AJ011794	Zea mays AUX1 protein. aux1.
SEQ ID NO: 740		
CAA65269.1	X96406	Solanum tuberosum 13-lipoxygenase.
AAB65767.1	U37840	Lycopersicon esculentum lipoxygenase. loxD. wound, systemin and methyl-jasmonate induced.
BAA03102.1	D14000	Oryza sativa lipoxygenase. lox2osPil.
AAC12951.1	U56406	Hordeum vulgare methyljasmonate-inducible lipoxygenase 2.
CAB94852.1	AJ404331	Prunus dulcis hydroperoxydation of polyunsaturated fatty acids. lipoxygenase. lox.
AAG21691.1	AY008278	Lycopersicon esculentum lipoxygenase. oxido-reductase.
AAA79186.1	U36339	Cucumis sativus lipoxygenase.
AAB67858.1	U60200	Solanum tuberosum lipoxygenase. POTLX-1. expressed during early tuberization.
CAA64765.1	X95512	Solanum tuberosum lipoxygenase.
CAB83038.1	AJ271161	Cucumis sativus oxygenase. lipoxygenase-9. lox9.
CAA58859.1	X84040	Nicotiana tabacum lipoxygenase. Lox1.
AAB67865.1	U60202	Solanum tuberosum lipoxygenase. POTLX-3. expressed in ABA-treated leaves.
CAA55724.1	X79107	Solanum tuberosum lipoxygenase. Lox1:St:1.
AAB67860.1	U60201	Solanum tuberosum lipoxygenase. POTLX-2. expressed during early tuberization.
CAB65460.1	Y18548	Solanum tuberosum lipoxygenase. lox1-St-2.

AAD04258.1	AF039651	Solanum tuberosum	5-lipoxygenase.
AAB81594.1	AF019613	Solanum tuberosum	lipoxygenase. plox1.
AAA33986.1	J02795	Glycine max	lipoxygenase-1.
AAB67732.1	U50075	Glycine max	lipoxygenase L-5. vlxB.
CAA47717.1	X67304	Glycine max	lipoxygenase.
AAB81595.1	AF019614	Solanum tuberosum	lipoxygenase. plox2.
CAA64766.1	X95513	Solanum tuberosum	lipoxygenase.
AAB31252.1	S73865	Solanum tuberosum	linoleate:oxygen oxidoreductase. linoleate:oxygen oxidoreductase, lipoxygenase, LOX. This sequence comes from Fig. 1; lipoxygenase; LOX.
AAA53184.1	U09026	Lycopersicon esculentum	lipoxygenase. loxA.
AAB65766.1	U37839	Lycopersicon esculentum	lipoxygenase. loxC. expressed during ripening fruit.
CAA65268.1	X96405	Solanum tuberosum	13-lipoxygenase.
AAF15296.2	AF204210	Phaseolus vulgaris	lipoxygenase. LOX4.
CAA55319.1	X78581	Pisum sativum	lipoxygenase. Lox1:Ps:3.
AAA03728.1	U04526	Glycine max	lipoxygenase.
CAA34906.1	X17061	Pisum sativum	lipoxygenase (AA 1-864).
CAA55318.1	X78580	Pisum sativum	lipoxygenase. Lox1:Ps:2.
BAA03042.1	D13949	Glycine max	lacking. lipoxygenase-2. lox2.
AAA33987.1	J03211	Glycine max	lipoxygenase (EC 1.13.11.12).
AAB71759.1	U84198	Pisum sativum	lipoxygenase. Lox1:Ps:1. expressed in root nodules.
AAB41272.1	U50081	Glycine max	lipoxygenase-3.
CAA39604.1	X56139	Glycine max	lipoxygenase. sc514.

AAA96817.1	U26457	Glycine max lipoygenase. vlxC.
AAG42354.1	AF234983	Phaseolus vulgaris lipoygenase.
AAG18376.1	AF283894	Zantedeschia aethiopica lipoygenase. lox2.
AAD39093.1	AF095895	Oryza sativa catalyzes the addition of molecular oxygen to fatty acid. lipoygenase. CM-LOX1.
CAC04380.1	AJ293015	Pisum sativum lipoygenase. lox1:Ps:7.
CAA45088.1	X63525	Phaseolus vulgaris lipoygenase. loxA.
AAB18970.2	U76687	Phaseolus vulgaris lipoygenase. PvLOX2.
AAC49159.1	U36191	Glycine max linoleate:oxygen oxidoreductase. lipoygenase. lox7.
AAA03726.1	U04785	Glycine max lipoygenase.
CAA45086.1	X63521	Phaseolus vulgaris lipoygenase.
SEQ ID NO: 741		
AAG28436.1	AF195029	Glycine max plasma membrane Ca <sup>2+</sup> -ATPase. SCA2.
AAG28435.1	AF195028	Glycine max plasma membrane Ca <sup>2+</sup> -ATPase. SCA1.
CAA68234.1	X99972	Brassica oleracea calmodulin-stimulated calcium-ATPase.
AAD31896.1	AF145478	Mesembryanthemum crystallinum calcium ATPase.
BAA90510.2	AP001111	Oryza sativa rice EST AU030811, similar to rice Ca <sup>2+</sup> -ATPase (U82966).
AAD11618.1	AF050496	Lycopersicon esculentum Ca <sup>2+</sup> -ATPase. LCA1B; alternative transcript.
AAD11617.1	AF050495	Lycopersicon esculentum Ca <sup>2+</sup> -ATPase. LCA1A; alternative transcript.
AAA34138.1	M96324	Lycopersicon esculentum The calcium ATPase is a calcium ion pump. Ca <sup>2+</sup> -ATPase. LCA1.
CAA63790.1	X93592	Dunaliella bioculata P-type ATPase. cal. calcium pumping; CA1.
AAF73985.1	AF096871	Zea mays calcium pump. calcium ATPase. cap1.

AAB58910.1	U82966	Oryza sativa	Ca <sup>2+</sup> -ATPase.
AAD46188.1	AF156691	Nicotiana plumbaginifolia	plasma membrane proton ATPase. pma9.
AAB17186.1	U72148	Lycopersicon esculentum	plasma membrane H <sup>+</sup> -ATPase. LHA4. plasma membrane proton pumping ATPase.
CAA47275.1	X66737	Nicotiana plumbaginifolia	plasma membrane H <sup>+</sup> -ATPase. pma4.
CAA54045.1	X76535	Solanum tuberosum	H(+)-transporting ATPase. PHA2.
AAD46186.1	AF156679	Nicotiana plumbaginifolia	plasma membrane proton ATPase. pma6.
CAA59800.1	X85805	Zea mays	H(+)-transporting ATPase. MHA-2.
BAA06629.1	D31843	Oryza sativa	plasma membrane H <sup>+</sup> -ATPase. OSA2.
AAB35314.2	S79323	Vicia faba	plasma membrane H(+)-ATPase precursor. plasma membrane H(+)-ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.
CAA59799.1	X85804	Phaseolus vulgaris	H(+)-transporting ATPase. BHA-1.
AAB41898.1	U84891	Mesembryanthemum crystallinum	plasma membrane proton pump. H <sup>+</sup> -transporting ATPase. PMA.
AAA34094.1	M80489	Nicotiana plumbaginifolia	plasma membrane H <sup>+</sup> ATPase. pma1.
AAB84202.2	AF029256	Kosteletzkya virginica	plasma membrane proton ATPase. ATP1.
AAA34052.1	M27888	Nicotiana plumbaginifolia	H <sup>+</sup> -translocating ATPase.
AAA34173.1	M60166	Lycopersicon esculentum	H <sup>+</sup> -ATPase. LHA1.
AAA34098.1	M80490	Nicotiana plumbaginifolia	plasma membrane H <sup>+</sup> ATPase. pma3.
AAF98344.1	AF275745	Lycopersicon esculentum	plasma membrane H <sup>+</sup> -ATPase. LHA2. P-type ion pump.
AAD55399.1	AF179442	Lycopersicon esculentum	plasma membrane H <sup>+</sup> -ATPase isoform LHA2. LHA2.
CAC29436.1	AJ310524	Vicia faba	P-type H <sup>+</sup> -ATPase. ha5. predominantly expressed in guard cells and flowers.
BAA08134.1	D45189	Zostera marina	plasma membrane H <sup>+</sup> -ATPase. zha1.

BAA01058.1	D10207	Oryza sativa	H-ATPase. OSA1.
CAB69824.1	AJ271439	Prunus persica	plasma membrane H <sup>+</sup> ATPase. PPA1.
CAA54046.1	X76536	Solanum tuberosum	H(+)-transporting ATPase. PHA1.
AAB60276.1	U09989	Zea mays	H(+)-transporting ATPase. Mha1.
CAB69823.1	AJ271438	Prunus persica	plasma membrane H <sup>+</sup> ATPase. PPA2.
AAK31799.1	AY029190	Lilium longiflorum	plasma membrane H <sup>+</sup> ATPase. LILHA1.
BAA37150.1	AB022442	Vicia faba	p-type H <sup>+</sup> -ATPase. VHA2.
CAC29435.1	AJ310523	Vicia faba	P-type H <sup>+</sup> -ATPase. vha4. predominantly expressed in flowers.
CAB85495.1	AJ132892	Medicago truncatula	proton pump. H <sup>+</sup> -ATPase. ha1.
CAB85494.1	AJ132891	Medicago truncatula	proton pump. H <sup>+</sup> -ATPase. ha1.
AAD46187.1	AF156683	Nicotiana plumbaginifolia	plasma membrane proton ATPase. pma8.
AAD29712.1	AF140499	Oryza sativa	chloroplast envelope calcium ATPase precursor.
AAK32118.1	AF308816	Hordeum vulgare	plasmalemma H <sup>+</sup> -ATPase 1.
AAG01028.1	AF289025	Cucumis sativus	plasma membrane H <sup>+</sup> -ATPase.
AAF97591.1	AF263917	Lycopersicon esculentum	plasma membrane proton ATPase. LHA8.
AAA81348.1	U38965	Vicia faba	p-type H <sup>+</sup> -ATPase. VHA2.
AAA20600.1	U08984	Zea mays	plasma-membrane H <sup>+</sup> ATPase. Zmpma1.
AAA20601.1	U08985	Zea mays	plasma-membrane H <sup>+</sup> ATPase. Zmpma1.
AAK32119.1	AF308817	Hordeum vulgare	plasmalemma H <sup>+</sup> -ATPase 2.
SEQ ID NO: 742			
AAD02548.1	AF049922	Petunia x hybrida	PGPS/D6. PGPS/D6. ER lumen protein retaining receptor homolog; putative HDEL receptor.
SEQ ID NO: 744			

AAG13424.1	AC051634	Oryza sativa	putative mitochondrial inner membrane protein. OSJNBb0018B10.5.
AAG46068.1	AC079830	Oryza sativa	putative inner mitochondrial membrane protein. OSJNBb0009F04.14.
SEQ ID NO: 746			
BAA32557.1	AB017159	Daucus carota	citrate synthase. DcCS.
AAA82743.1	U19481	Citrus maxima	synthesis of citrate from oxaloacetate and acetylCoA. citrate synthase precursor. cit.
AAG28777.1	AF302906	Oryza sativa	citrate synthase. similar to putative Oryza sativa citrate synthase in GenBank Accession Number AC004521.
CAA59008.1	X84226	Nicotiana tabacum	citrate synthase. cit1.
CAA52976.1	X75082	Solanum tuberosum	mitochondrial citrate-synthase. ethanolamine ammonia-lyase.
BAA82390.1	AP000367	Oryza sativa	ESTs C96653(C10531),C96654(C10531),C28571(C61641) correspond to a region of the predicted gene.; Similar to citrate synthetase. (AC004521).
CAA59010.1	X84228	Beta vulgaris	citrate (si)-synthase. cit1.
CAA59009.1	X84227	Populus x generosa	citrate (si)-synthase. cit1.
BAA07328.1	D38132	Cucurbita sp.	conversion of oxaloacetate to citrate in the glyoxylate cycle. glyoxysomal citrate synthase.
SEQ ID NO: 750			
AAA85365.1	L42466	Picea glauca	ethylene-forming enzyme. EFE.
AAC95363.1	AF104925	Solanum chacoense	2-oxoglutarate-dependent dioxygenase. SPP2. pollination and fertilization induced gene.
BAA75309.1	AB023790	Ipomoea batatas	flavanone 3-hydroxylase. f3h III.
BAA75308.1	AB023789	Ipomoea batatas	flavanone 3-hydroxylase. f3h II.
BAA75306.1	AB023787	Ipomoea batatas	anthocyanidin synthase. ans II.
AAC48922.1	U06047	Vigna radiata	1-aminocyclopropane-1-carboxylate oxidase homolog.
SEQ ID NO: 751			
BAB40010.1	AP003021	Oryza sativa	putative wall-associated kinase 2. P0503E05.12.
BAA95893.1	AP002071	Oryza sativa	Similar to Arabidopsis thaliana wak4 gene; wall-associated kinase 4. (AJ009695).

BAB40015.1	AP003021	Oryza sativa	putative wall-associated kinase 1. P0503E05.18.
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
BAB40021.1	AP003021	Oryza sativa	putative wall-associated kinase 2. P0503E05.25. contains EST C24950(S16264).
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
AAB09771.1	U67422	Zea mays	CRINKLY4 precursor. cr4. receptor kinase homolog.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK11566.1	AF318490	Lycopersicon hirsutum	Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAB40022.1	AP003021	Oryza sativa	putative wall-associated kinase 1. P0503E05.26.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
AAF76313.1	AF220603	Lycopersicon esculentum	Pto kinase. LescPth5.
AAB47421.1	U59316	Lycopersicon esculentum	serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.

AAB47423.1	U59315	Lycopersicon pimpinellifolium	serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
AAC48914.1	U02271	Lycopersicon pimpinellifolium	protein kinase.
AAF76306.1	AF220602	Lycopersicon pimpinellifolium	Pto kinase.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
AAK11567.1	AF318491	Lycopersicon hirsutum	Pto-like protein kinase F. LhirPtoF.
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
AAK11569.1	AF318493	Lycopersicon hirsutum	Pto-like protein kinase D. LhirPtoD.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAA83373.1	AP000391	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
BAA84787.1	AP000559	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
AAK11568.1	AF318492	Lycopersicon hirsutum	Pto-like protein kinase B. LhirPtoB.
BAA78764.1	AB023482	Oryza sativa	ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).



AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
AAK31267.1	AC079890	Oryza sativa	putative protein kinase. OSJNBb0089A17.2.
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
SEQ ID NO: 752			
BAB39155.1	AB048713	Pisum sativum	SCARECROW. PsSCR.
AAG13663.1	AF263457	Zea mays	transcription factor. SCARECROW. SCR. ZmSCR.
BAA90816.1	AP001168	Oryza sativa	Similar to SCARECROW (U62798).
AAC98090.1	AF067400	Zea mays	Sc11 protein. Sc11. Scarecrow-like; similar to Zea mays sequence presented in GenBank Accession Number T18310.
BAB39156.1	AB048714	Pisum sativum	SCARECROW. PsSCR.
SEQ ID NO: 753			
AAF21901.1	AF109392	Brassica napus	ligand gated channel-like protein. glutamate receptor homolog.
SEQ ID NO: 757			
CAA92821.1	Z68504	Oryza sativa	3-hydroxy-3-methylglutaryl-CoA reductase.
AAA33360.1	M74800	Hevea brasiliensis	3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
CAA70440.1	Y09238	Zea mays	3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAB69727.1	U72146	Camptotheca acuminata	3-hydroxy-3-methylglutaryl coenzyme A reductase. converts HMGCoA in mevalonate precursor for isoprenoid compounds; HMGR; hmgr2; similar to protein encoded by GenBank Accession Number L10390.
AAD08820.1	U43961	Oryza sativa	3-hydroxy-3-methylglutaryl=CoA reductase. HMGR.
AAA68965.1	U14624	Artemisia annua	3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM1.
AAD47596.1	AF142473	Artemisia annua	HMG-CoA reductase. HMGR1.
AAD03789.1	U43711	Morus alba	catalyzes the final step in mevalonate pathway. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR.

AAA33108.1	M96068	Catharanthus roseus	hydroxymethylglutaryl-CoA reductase. HMGR.
CAA48610.1	X68651	Raphanus sativus	hydroxymethylglutaryl-CoA reductase (NADPH). HMG1.
AAA93498.1	L01400	Solanum tuberosum	convert HMG-CoA into mevalonate. hydroxymethylglutaryl coenzyme A reductase. hmgr. putative.
AAA68966.1	U14625	Artemisia annua	3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM4.
AAB52552.1	U51986	Solanum tuberosum	HMG-CoA reductase.
CAA48611.1	X68652	Raphanus sativus	hydroxymethylglutaryl-CoA reductase (NADPH). HMG2.
BAA93631.1	AB022690	Solanum tuberosum	3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG3.
AAB62581.1	U68072	Lycopersicon esculentum	3-hydroxy-3-methylglutaryl CoA reductase 2. HMG2.
AAA34169.1	M63642	Lycopersicon esculentum	3-hydroxy-3-methylglutaryl coenzyme A reductase. hmg2.
AAB69726.1	U72145	Camptotheca acuminata	converts HMGC <sub>o</sub> A to mevalonate. 3-hydroxy-3-methylglutaryl coenzyme a reductase. hmg3. HMGR.
AAB52551.1	U51985	Solanum tuberosum	HMG-CoA reductase.
AAA33040.1	L10390	Camptotheca acuminata	3-hydroxy-3-methylglutaryl coA reductase.
AAD28179.1	AF110383	Capsicum annuum	3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR2M. HMGR.
BAB20771.1	AB041031	Solanum tuberosum	3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG2.
AAB53748.1	U95816	Oryza sativa	3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.
AAC05088.1	AF038045	Gossypium hirsutum	catalyzes the synthesis of mevalonate from hmg-coA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1. hmg1. hmg-coA reductase 1; HMGR1.
CAA45181.1	X63649	Nicotiana sylvestris	catalyses synthesis of mevalonate. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR. endoplasmic reticulum location.
CAA38469.1	X54659	Hevea brasiliensis	hydroxymethylglutaryl-CoA reductase. HMGR1.
CAA38467.1	X54657	Hevea brasiliensis	hydroxymethylglutaryl-CoA reductase. HMGR1.

AAD38873.1	AF110382	Oryza sativa	3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR3G. HMG-CoA reductase.
BAA36291.1	AB021862	Cucumis melo	HMG-CoA reductase. Cm-HMGR. putative.
AAB87727.1	U60452	Nicotiana tabacum	hydroxy-methylglutaryl-coenzyme A reductase. HMGR1.
AAC05089.1	AF038046	Gossypium hirsutum	catalyzes the synthesis of mevalonate from hmg-coA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2. hmg2. hmg-coA reductase 2; HMGR2.
AAC15475.1	AF034760	Tagetes erecta	3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAC15476.1	AF034761	Tagetes erecta	3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAA21720.1	L28995	Oryza sativa	conversion of hydroxymethylglutaryl coenzyme A to mevalonate. 3-hydroxy-3-methylglutaryl coenzyme A reductase. putative.
AAA33358.1	M74798	Hevea brasiliensis	3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
AAC72378.1	AF096838	Solanum tuberosum	3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAB04043.1	L40938	Lycopersicon esculentum	HMGR CoA reductase. HMGR1.
CAA38468.1	X54658	Hevea brasiliensis	hydroxymethylglutaryl-CoA reductase. HMGR2.
CAA52787.1	X74783	Lithospermum erythrorhizon	3-hydroxy-3-methyl glutaryl coenzyme A reductase. Lehmgr1.
AAD09278.1	U97683	Glycine max	catalyzes the synthesis of mevalonate, the specific precursor of all isoprenoid compounds present in plants. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMG-CoA reductase.
AAG43469.1	AF196964	Bixa orellana	catalyzes mevalonate synthesis from hmg-CoA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase.
BAA09705.1	D63389	Cucumis sativus	3-hydroxy-3-methylglutaryl CoA reductase.
AAB47161.1	S82272	Gossypium barbadense	3-hydroxy-3-methylglutaryl coenzyme A reductase. /gene="3-hydroxy-3-methylglutaryl coenzyme A reductase,. This sequence comes from Fig. 2; 3-hydroxy-3-methylglutaryl CoA reductase; HMGR.
AAA33359.1	M74799	Hevea brasiliensis	3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
AAC37434.1	L34827	Solanum tuberosum	HMG-CoA reductase. hmg1 gene family.

AAC37432.1	L34825	Solanum tuberosum	HMG-CoA reductase. hmg1 gene family.
AAC37435.1	L34828	Solanum tuberosum	HMG-CoA reductase. hmg1 gene family.
AAC37433.1	L34826	Solanum tuberosum	HMG-CoA reductase. hmg1 gene family.
AAC37431.1	L34823	Solanum tuberosum	HMG-CoA reductase. hmg1 gene family.
SEQ ID NO: 761			
CAA96512.1	Z71980	Malus x domestica	knotted1-like homeobox protein.
BAA25921.1	AB004797	Nicotiana tabacum	NTH23. homeobox gene.
AAD09582.1	U76409	Lycopersicon esculentum	homeobox 1 protein. THox1. homeodomain protein.
AAC49918.1	AF000142	Lycopersicon esculentum	class II knotted-like homeodomain protein. LeT12.
BAA08552.1	D49704	Oryza sativa	OSH45. OSH44 transcript homeobox gene.
BAB18585.1	AB043957	Ceratopteris richardii	CRKNOX3. crknox3. knotted1-like homeodomain protein.
AAD00253.1	U76410	Lycopersicon esculentum	homeobox 2 protein. THox2. homeodomain protein.
CAA82314.1	Z29073	Brassica napus	homeodomain-containing protein. Bnhd1.
BAA77822.1	AB007628	Oryza sativa	HOS59. homeobox gene.
BAA77823.1	AB007629	Oryza sativa	HOS66. homeobox gene.
AAB81079.1	AF022390	Hordeum vulgare	knotted class 1 homeodomain protein. k. similar to the hooded gene product encoded by GenBank Accession Number X83518; similar to the maize knotted-1 gene product encoded by GenBank Accession Number X61308.
AAF32399.1	AF224499	Triticum aestivum	KNOTTED-1-like homeobox protein b. knox1b. KNOX1b.
BAA76750.1	AB025573	Nicotiana tabacum	KN1-type homeobox protein. NTH1.
AAF32400.1	AF224500	Triticum aestivum	KNOTTED-1-like homeobox protein d. knox1d. KNOX1d.
AAC49917.1	AF000141	Lycopersicon esculentum	class I knotted-like homeodomain protein. LeT6.
BAA25546.1	AB004785	Nicotiana tabacum	NTH15. homeobox gene.

AAF32398.1	AF224498	<i>Triticum aestivum</i>	KNOTTED-1-like homeobox protein a. knox1a. KNOX1.
AAD13611.1	AF100455	<i>Zea mays</i>	knotted class 1 homeodomain protein liguleless3. lg3.
AAC84001.1	AF063248	<i>Picea abies</i>	homeobox protein.
AAC33008.1	AF080104	<i>Pisum sativum</i>	knotted1-like class I homeodomain protein. PsKn1.
AAD00692.1	U90092	<i>Picea mariana</i>	homeobox transcription factor SKN2. knotted1-like homeobox gene.
AAC32262.1	AF063307	<i>Pisum sativum</i>	Knox class 1 protein. Hop1.
BAA03959.1	D16507	<i>Oryza sativa</i>	homeobox protein. OSH1.
AAG27464.1	AF308454	<i>Medicago truncatula</i>	knotted class I homeodomain KNOX.
AAD00691.1	U90091	<i>Picea mariana</i>	homeobox transcription factor SKN1. knotted1-like homeobox gene.
AAC32817.1	AF050180	<i>Oryza sativa</i>	transcription factor. KNOX class homeodomain protein. Oskn2.
BAA79226.1	AB028885	<i>Oryza sativa</i>	knotted1-type homeobox protein OSH71. OSH71.
BAA79224.1	AB028883	<i>Oryza sativa</i>	knotted1-type homeobox protein OSH6. OSH6.
BAA77818.1	AB007624	<i>Oryza sativa</i>	HOS9. homeobox gene.
BAB19772.1	AP002881	<i>Oryza sativa</i>	putative knotted1-type homeobox protein. P0035H10.13.
AAF23753.2	AF193813	<i>Brassica oleracea</i>	shoot meristemless. Stm. homeodomain protein.
AAD00251.1	U76407	<i>Lycopersicon esculentum</i>	knotted 2 protein. TKn2. homeodomain protein.
CAA96510.1	Z71978	<i>Malus x domestica</i>	kn1-like protein.
BAA31688.1	AB016071	<i>Oryza sativa</i>	OSH15. homeobox gene.
BAA77817.1	AB007623	<i>Oryza sativa</i>	HOS3. homeobox gene.
BAB18582.1	AB043954	<i>Ceratopteris richardii</i>	CRKNOX1. crknx1. knotted1-like homeodomain protein.
BAA76903.1	AB025713	<i>Nicotiana tabacum</i>	homeobox 9. NTH9.

AAD00252.1 U76408 *Lycopersicon esculentum*  
knotted 3 protein. TKn3. homeodomain protein.

BAB18584.1 AB043956 *Ceratopteris richardii*  
CRKNOX2. crknox2. knotted1-like homeodomain protein.

CAA96511.1 Z71979 *Malus x domestica*  
kn1-like protein.

AAA20882.1 L13663 *Glycine max*  
SBH1. Sbh1. soybean homeobox-containing gene.

CAB88029.1 AJ276389 *Dendrobium grex Madame Thong-In*  
transcription factor. knotted1-like homeobox protein.

SEQ ID NO: 762

AAB65776.1 U97521 *Vitis vinifera*  
class IV endochitinase. VvChi4A.

AAB65777.1 U97522 *Vitis vinifera*  
class IV endochitinase. VvChi4B.

CAA53626.1 X76041 *Triticum aestivum*  
endochitinase. CHI.

AAG53609.1 AF280437 *Secale cereale*  
31.7 kDa class I endochitinase-antifreeze protein precursor. cht9.

BAA03750.1 D16222 *Oryza sativa*  
endochitinase. Cht-2.

AAA32986.1 M95835 *Brassica napus*  
endochitinase. Ch25.

BAA03749.1 D16221 *Oryza sativa*  
endochitinase. Cht-1.

AAB01895.1 U48687 *Castanea sativa*  
endochitinase.

SEQ ID NO: 763

AAA34065.1 M94135 *Nicotiana tabacum*  
chloroplast carbonic anhydrase.

AAA34057.1 L19255 *Nicotiana tabacum*  
carbonic anhydrase.

AAB65822.1 U55838 *Populus tremula x Populus tremuloides*  
carbonic anhydrase. CA1b. EC 4.2.1.1.

AAC49785.1 U55837 *Populus tremula x Populus tremuloides*  
carbonic anhydrase. CA1a. EC 4.2.1.1.

AAA34026.1 M27295 *Spinacia oleracea*  
carbonic anhydrase precursor.

AAA34027.1 J05403 *Spinacia oleracea*  
carbonic anhydrase (EC 4.2.1.1).

AAA86993.1 U19738 *Flaveria linearis*  
reversible hydration of carbon dioxide. carbonic anhydrase 1.

AAA86942.1	U08402	Flaveria brownii	carbonic anhydrase.
AAA86992.1	U19737	Flaveria pringlei	reversible hydration of carbon dioxide. carbonic anhydrase.
AAA86939.1	U08398	Flaveria bidentis	carbonic anhydrase.
AAD27876.2	AF139464	Vigna radiata	carbonic anhydrase. CipCa1.
AAA33652.1	M63627	Pisum sativum	carbonic anhydrase.
AAD29050.1	AF132855	Gossypium hirsutum	interconversion of CO <sub>2</sub> and HCO <sub>3</sub> <sup>-</sup> . carbonic anhydrase isoform 2. CA2. zinc metalloenzyme; carbonate dehydratase.
AAD29049.1	AF132854	Gossypium hirsutum	interconversion of CO <sub>2</sub> and HCO <sub>3</sub> <sup>-</sup> . carbonic anhydrase isoform 1. CA1. zinc metalloenzyme; carbonate dehydratase.
AAA86994.1	U19740	Flaveria linearis	reversible hydration of carbon dioxide. carbonic anhydrase 2.
CAB43571.1	AJ239132	Glycine max	hydration of carbon dioxide. carbonic anhydrase. ca1.
CAA63712.1	X93312	Medicago sativa	Carbonic anhydrase. ca1.
AAA86945.1	U08403	Zea mays	carbonic anhydrase.
AAA86944.1	U08401	Zea mays	carbonic anhydrase.
AAC41656.1	L36959	Hordeum vulgare	carbonic anhydrase. putative.
AAA86943.1	U08404	Oryza sativa	carbonic anhydrase. nuclear encoded, localized to chloroplast.
AAD56038.1	AF182806	Oryza sativa	carbonic anhydrase 3. ca3.
BAA31953.1	AB016283	Oryza sativa	carbonic anhydrase.
AAA69027.1	U19739	Urochloa panicoides	reversible hydration of carbon dioxide. carbonic anhydrase 2.
AAA69028.1	U19741	Urochloa panicoides	reversible hydration of carbon dioxide. carbonic anhydrase 1.
BAA95793.1	AB009887	Nicotiana tabacum	carbonic anhydrase. carbonic anhydrase.
AAF78507.1	AF195204	Pyrus pyrifolia	carbonic anhydrase isoform 1. CA1.

AAC33484.1	U49976	Coccomyxa sp. PA	beta-type carbonic anhydrase beta-CA1.
AAA18560.1	M95073	Zea mays	putative. silimar to carbonic anhydrases.
AAB19184.1	U41190	Chlamydomonas reinhardtii	carbonic anhydrase precursor. beta-CA2.
AAB19183.1	U41189	Chlamydomonas reinhardtii	carbonic anhydrase precursor. beta-CA1.
AAC49887.1	U80804	Chlamydomonas reinhardtii	beta-carbonic anhydrase. ca1. beta-CA1.
AAC49888.1	U80805	Chlamydomonas reinhardtii	beta-carbonic anhydrase. ca2. beta-CA2.
SEQ ID NO: 764			
AAC06027.1	AF052058	Vigna unguiculata	iron storage and mobilization in plants. ferritin subunit cowpea2 precursor.
AAD50644.1	AF133814	Solanum tuberosum	ferritin 1. F1.
AAB53099.1	U68217	Brassica napus	iron binding protein. ferritin. LSC30.
AAA33959.1	M64337	Glycine max	ferritin light chain. ferritin.
AAA34016.1	M72894	Glycine max	ferritin light chain. SOF-H2.
CAA58146.1	X83076	Zea mays	ferritin. Fer1.
AAB18928.1	U31648	Glycine max	iron storage protein. ferritin.
CAA65771.1	X97059	Medicago sativa	iron storage. ferritin. FER. abscissic acid regulated.
CAA43663.1	X61391	Zea mays	ferritin.
CAA58147.1	X83077	Zea mays	ferritin. Fer2.
AAC06026.1	AF052057	Vigna unguiculata	iron storage and mobilization in plants. ferritin subunit cowpea3 precursor.
CAA43664.1	X61392	Zea mays	ferritin.
CAA51786.1	X73369	Pisum sativum	ferritin.
CAA45763.1	X64417	Pisum sativum	ferritin-precursor.



CAA41213.1	X58274	Phaseolus vulgaris ferritin. pfe.
AAA33958.1	M58336	Glycine max ferritin light chain. SOF-5L.
CAB42587.1	AJ238628	Chlorella protothecoides putative ferritin. dee188.
BAB17852.1	AB042612	Nicotiana tabacum ferritin 1. tob-fer-1. putative.
AAC15241.1	AF028072	Pinus taeda ferritin.
CAA47983.1	X67755	Vigna unguiculata ferritin 2. pfe2.
CAA47982.1	X67754	Vigna unguiculata ferritin 1. pfe1.
CAA47984.1	X67756	Vigna unguiculata ferritin 5. pfe5.
AAC12282.1	AF052511	Glycine max iron storage and mobilization. ferritin 2. soybean 2; cowpea 2 homolog.
AAC12281.1	AF052513	Glycine max iron storage and mobilization. ferritin 1. soybean 1; cowpea 1 homolog.
SEQ ID NO: 765		
AAC36697.1	AF075579	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
CAC10358.1	AJ277086	Nicotiana tabacum protein phosphatase 2C. PP2C1.
CAB90633.1	AJ277743	Fagus sylvatica protein phosphatase 2C (PP2C). pp2C1. ABA-induced protein.
AAD17804.1	AF092431	Lotus japonicus nodule-enhanced protein phosphatase type 2C. NPP2C1.
CAC10359.1	AJ277087	Nicotiana tabacum protein phosphatase 2C. PP2C2.
CAC09575.1	AJ298987	Fagus sylvatica protein phosphatase 2C (PP2C). pp2Cf1.
CAA72341.1	Y11607	Medicago sativa protein phosphatase 2C. MP2C.
CAB61839.1	AJ242803	Sporobolus stapfianus putative serine/threonine phosphatase type 2c.
AAD17805.1	AF092432	Lotus japonicus protein phosphatase type 2C. PP2C2.
AAG43835.1	AF213455	Zea mays protein phosphatase type-2C. pp2c-1. PP2C-1.

AAG46118.1	AC073166	Oryza sativa	putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-Lys.
AAG13599.1	AC051633	Oryza sativa	putative protein phosphatase-2C. OSJNBb0015I11.26.
AAC36698.1	AF075580	Mesembryanthemum crystallinum	protein phosphatase-2C. PP2C.
BAB12036.1	AP002820	Oryza sativa	putative protein phosphatase. P0702D12.18.
AAC36700.1	AF075582	Mesembryanthemum crystallinum	protein phosphatase-2C. PP2C.
AAC36699.1	AF075581	Mesembryanthemum crystallinum	protein phosphatase-2C. PP2C.
AAK20060.1	AC025783	Oryza sativa	putative protein phosphatase 2C. OSJNBa0001O14.1.
AAD11430.1	AF097667	Mesembryanthemum crystallinum	protein phosphatase 2C homolog. PP2C.
CAB90634.1	AJ277744	Fagus sylvatica	protein phosphatase 2C (PP2C). pp2C2. ABA and calcium induced protein.
AAC35951.1	AF079355	Mesembryanthemum crystallinum	protein phosphatase-2c. PP2C.
AAF19804.1	AF180355	Brassica oleracea	ABI1 protein. ABI1. similar to Arabidopsis thaliana ABI1.
AAB93832.1	U81960	Zea mays	kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases; type 2C protein phosphatase. kinase associated protein phosphatase. KAPP.
AAC26828.1	AF075603	Oryza sativa	kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases. kinase associated protein phosphatase. kapp. type 2C protein phosphatase.
CAC09576.1	AJ298988	Fagus sylvatica	protein phosphatase 2C (PP2C). pp2Cf2.
SEQ ID NO: 766			
AAG08959.1	AF122051	Solanum tuberosum	tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAG08960.1	AF122052	Solanum tuberosum	tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAG08961.1	AF122053	Solanum tuberosum	tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.

BAA88169.1	AP000836	Oryza sativa	Similar to putative transcription factor (AF062890).
BAA88205.1	AP000837	Oryza sativa	Similar to putative transcription factor (AF062890).
AAF34434.1	AF172282	Oryza sativa	myb-like protein. DUPR11.29.
AAF78890.1	AF189788	Hordeum vulgare	putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.
AAF78889.1	AF189787	Hordeum vulgare	putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.
AAF67053.1	AF190304	Adiantum raddianum	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF67052.1	AF190303	Adiantum raddianum	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF78888.1	AF189786	Physcomitrella patens	putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.
AAF78887.1	AF189785	Physcomitrella patens	putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.
AAF43043.1	AF236059	Papaver rhoeas	putative Myb-related domain. pmr.
BAA94769.1	AP001859	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4, BAC clone F4D11; putative myb-protein. (AL022537).
AAF67050.1	AF190301	Secale cereale	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF67051.1	AF190302	Secale cereale	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
CAA78388.1	Z13998	Petunia x hybrida	DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb proto-oncoproteins.
BAB39987.1	AP003020	Oryza sativa	putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
BAB39972.1	AP003018	Oryza sativa	putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).
CAA72218.1	Y11415	Oryza sativa	myb.
BAA81731.1	AB029160	Glycine max	GmMYB29A1.
BAA81730.1	AB029159	Glycine max	GmMYB29A1.

CAA72217.1	Y11414	Oryza sativa	myb.
BAA81736.1	AB029165	Glycine max	GmMYB29B2.
BAB12688.1	AP002746	Oryza sativa	putative MYB family transcription factor. P0671B11.3. contains ESTs AU082307(E0784),C72014(E0784).
BAA99440.1	AP002743	Oryza sativa	putative MYB family transcription factor. P0710E05.27. contains ESTs AU082307(E0784),C72014(E0784).
AAB41101.1	U72762	Nicotiana tabacum	transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.
BAA88223.1	AB028651	Nicotiana tabacum	myb-related transcription factor LBM3. lbm3.
BAA23340.1	D88620	Oryza sativa	transfactor. OSMYB4. Osmbyb4.
BAA93038.1	AP001552	Oryza sativa	EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).
AAA33067.1	L04497	Gossypium hirsutum	MYB A; putative.
BAA81733.2	AB029162	Glycine max	GmMYB29A2.
BAA88222.1	AB028650	Nicotiana tabacum	myb-related transcription factor LBM2. lbm2.
CAB43399.1	AJ006292	Antirrhinum majus	Myb-related transcription factor mixta-like 1. mybml1.
BAA81732.1	AB029161	Glycine max	GmMYB29A2.
AAG28525.1	AF198498	Nicotiana tabacum	anther-specific myb-related protein 2. mybAS2. NtMYBAS2; contains tandem R2, R3 myb domains similar to c-myb family.
CAA50226.1	X70881	Hordeum vulgare	MybHv33. myb3.
CAA50223.1	X70878	Hordeum vulgare	MybHv33. myb3.
CAA78387.1	Z13997	Petunia x hybrida	DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
CAA67000.1	X98355	Oryza sativa	activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.

AAK19616.1	AF336283	Gossypium hirsutum	GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.
AAG28526.1	AF198499	Nicotiana tabacum	anther-specific myb-related protein 1. mybAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.
CAA78386.1	Z13996	Petunia x hybrida	DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
CAA66952.1	X98308	Lycopersicon esculentum	THM18. myb-related transcription factor.
BAA23341.1	D88621	Oryza sativa	transfactor. OSMYB5. Osmyb5.
CAA50221.1	X70876	Hordeum vulgare	MybHv5. myb2.
AAK19611.1	AF336278	Gossypium hirsutum	BNLGH1233. bnlghi6233. similar to myb.
AAC04716.1	AF034130	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-D. similar to MYB A encoded by GenBank Accession Number L04497.
CAA61021.1	X87690	Hordeum vulgare	transcriptional activator of alpha-amylase gene promoter. GAMyb protein. Gam1.
AAG22863.1	AY008692	Hordeum vulgare	transcription factor GAMyb. Gamyb.
SEQ ID NO: 767			
CAB08111.1	Z94180	Lycopersicon esculentum	branched chain alpha-keto acid dehydrogenase E1-alpha subunit.
CAA81558.1	Z26949	Solanum tuberosum	subunit of the mitochondrial pyruvate dehydrogenase complex. E1 alpha subunit of pyruvate dehydrogenase precursor.
AAC72195.1	AF069911	Zea mays	pyruvate dehydrogenase E1 alpha subunit.
AAG43499.1	AF209924	Lycopersicon esculentum	pyruvate dehydrogenase.
AAA97411.1	U51918	Pisum sativum	pyruvate dehydrogenase E1 alpha subunit.
CAA10992.1	AJ222787	Hordeum vulgare	alpha-keto acid dehydrogenase-like protein. homology to branched chain alpha-keto acid dehydrogenase E1-alpha subunit.
SEQ ID NO: 768			
AAF64450.1	AF239928	Euphorbia esula	glutathione S-transferase. similar to auxin-inducible GST.

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AAG16758.1 AY007560 *Lycopersicon esculentum*  
putative glutathione S-transferase T3.

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AAG34803.1 AF243368 *Glycine max*  
glutathione S-transferase GST 13.

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AAG16756.1 AY007558 *Lycopersicon esculentum*  
putative glutathione S-transferase T1.

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AAG34796.1 AF243361 *Glycine max*  
glutathione S-transferase GST 6.

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AAG34809.1 AF243374 *Glycine max*  
glutathione S-transferase GST 19.

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AAG34797.1 AF243362 *Glycine max*  
glutathione S-transferase GST 7.

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AAG34807.1 AF243372 *Glycine max*  
glutathione S-transferase GST 17.

---

AAG34798.1 AF243363 *Glycine max*  
glutathione S-transferase GST 8.

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AAG34804.1 AF243369 *Glycine max*  
glutathione S-transferase GST 14.

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AAG16759.1 AY007561 *Lycopersicon esculentum*  
putative glutathione S-transferase T4.

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AAG34801.1 AF243366 *Glycine max*  
glutathione S-transferase GST 11.

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AAG34810.1 AF243375 *Glycine max*  
glutathione S-transferase GST 20.

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AAG16757.1 AY007559 *Lycopersicon esculentum*  
putative glutathione S-transferase T2.

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AAC18566.1 AF048978 *Glycine max*  
2,4-D inducible glutathione S-transferase. GSTa.

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AAG34808.1 AF243373 *Glycine max*  
glutathione S-transferase GST 18.

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AAG34800.1 AF243365 *Glycine max*  
glutathione S-transferase GST 10.

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CAA71784.1 Y10820 *Glycine max*  
glutathione transferase.

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AAG34844.1 AF244701 *Zea mays*  
glutathione S-transferase GST 36.

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AAG32472.1 AF309379 *Oryza sativa* subsp. *japonica*  
putative glutathione S-transferase OsGSTU3.

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AAA68430.1 J03679 *Solanum tuberosum*  
glutathione S-transferase. *gst1*. previously called pathogenesis-related protein; *prp1-1*.

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CAA04391.1 AJ000923 *Carica papaya*  
glutathione transferase. PGST1.

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AAG34831.1	AF244688	<i>Zea mays</i> glutathione S-transferase GST 23.
CAA09187.1	AJ010448	<i>Alopecurus myosuroides</i> glutathione transferase. GST1a.
CAA09188.1	AJ010449	<i>Alopecurus myosuroides</i> glutathione transferase. GST1b.
AAG34802.1	AF243367	<i>Glycine max</i> glutathione S-transferase GST 12.
AAG34805.1	AF243370	<i>Glycine max</i> glutathione S-transferase GST 15.
AAG34832.1	AF244689	<i>Zea mays</i> glutathione S-transferase GST 24.
AAG34837.1	AF244694	<i>Zea mays</i> glutathione S-transferase GST 29.
AAG34836.1	AF244693	<i>Zea mays</i> glutathione S-transferase GST 28.
AAG32471.1	AF309378	<i>Oryza sativa</i> subsp. <i>japonica</i> putative glutathione S-transferase OsGSTU4.
AAG34849.1	AF244706	<i>Zea mays</i> glutathione S-transferase GST 41.
CAC24549.1	AJ296343	<i>Cichorium intybus</i> x <i>Cichorium endivia</i> glutathione S-transferase. chi-GST1. auxin-induced GST.
AAC32118.1	AF051214	<i>Picea mariana</i> probable glutathione S-transferase. Sb18. similar to <i>Nicotiana tabacum</i> probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAG34795.1	AF243360	<i>Glycine max</i> glutathione S-transferase GST 5.
AAG34841.1	AF244698	<i>Zea mays</i> glutathione S-transferase GST 33.
AAF29773.1	AF159229	<i>Gossypium hirsutum</i> glutathione S-transferase. GST.
SEQ ID NO: 769		
AAG34797.1	AF243362	<i>Glycine max</i> glutathione S-transferase GST 7.
AAG34798.1	AF243363	<i>Glycine max</i> glutathione S-transferase GST 8.
AAG34803.1	AF243368	<i>Glycine max</i> glutathione S-transferase GST 13.
AAG16758.1	AY007560	<i>Lycopersicon esculentum</i> putative glutathione S-transferase T3.
AAF64450.1	AF239928	<i>Euphorbia esula</i> glutathione S-transferase. similar to auxin-inducible GST.

AAG34801.1	AF243366	Glycine max glutathione S-transferase GST 11.
AAG34804.1	AF243369	Glycine max glutathione S-transferase GST 14.
AAG34796.1	AF243361	Glycine max glutathione S-transferase GST 6.
AAG34809.1	AF243374	Glycine max glutathione S-transferase GST 19.
AAG16759.1	AY007561	Lycopersicon esculentum putative glutathione S-transferase T4.
AAG16757.1	AY007559	Lycopersicon esculentum putative glutathione S-transferase T2.
AAG16756.1	AY007558	Lycopersicon esculentum putative glutathione S-transferase T1.
AAG34807.1	AF243372	Glycine max glutathione S-transferase GST 17.
AAG34810.1	AF243375	Glycine max glutathione S-transferase GST 20.
AAG34844.1	AF244701	Zea mays glutathione S-transferase GST 36.
AAG34831.1	AF244688	Zea mays glutathione S-transferase GST 23.
AAC18566.1	AF048978	Glycine max 2,4-D inducible glutathione S-transferase. GSTa.
AAG34832.1	AF244689	Zea mays glutathione S-transferase GST 24.
AAG34808.1	AF243373	Glycine max glutathione S-transferase GST 18.
AAG34837.1	AF244694	Zea mays glutathione S-transferase GST 29.
AAG34800.1	AF243365	Glycine max glutathione S-transferase GST 10.
AAG34836.1	AF244693	Zea mays glutathione S-transferase GST 28.
CAA04391.1	AJ000923	Carica papaya glutathione transferase. PGST1.
CAA71784.1	Y10820	Glycine max glutathione transferase.
AAG34849.1	AF244706	Zea mays glutathione S-transferase GST 41.
AAA68430.1	J03679	Solanum tuberosum glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.



AAG34802.1	AF243367	Glycine max glutathione S-transferase GST 12.
CAC24549.1	AJ296343	Cichorium intybus x Cichorium endivia glutathione S-transferase. chi-GST1. auxin-induced GST.
CAA09187.1	AJ010448	Alopecurus myosuroides glutathione transferase. GST1a.
AAF22518.1	AF118925	Papaver somniferum glutathione S-transferase 2. GST2.
AAG32471.1	AF309378	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU4.
CAA09188.1	AJ010449	Alopecurus myosuroides glutathione transferase. GST1b.
AAF22517.1	AF118924	Papaver somniferum glutathione S-transferase 1. GST1.
AAF22647.1	AF193439	Lycopersicon esculentum glutathione S-transferase/peroxidase. BI-GST/GPX.
AAG32473.1	AF309380	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU2.
AAG32472.1	AF309379	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU3.
SEQ ID NO: 771		
AAG46118.1	AC073166	Oryza sativa putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-Lys.
AAG13599.1	AC051633	Oryza sativa putative protein phosphatase-2C. OSJNBb0015I11.26.
BAB12036.1	AP002820	Oryza sativa putative protein phosphatase. P0702D12.18.
AAC36698.1	AF075580	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
CAA72341.1	Y11607	Medicago sativa protein phosphatase 2C. MP2C.
AAG43835.1	AF213455	Zea mays protein phosphatase type-2C. pp2c-1. PP2C-1.
CAB61839.1	AJ242803	Sporobolus stapfianus putative serine/threonine phosphatase type 2c.
AAD17804.1	AF092431	Lotus japonicus nodule-enhanced protein phosphatase type 2C. NPP2C1.
AAD17805.1	AF092432	Lotus japonicus protein phosphatase type 2C. PP2C2.
AAC36697.1	AF075579	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.

CAB90633.1	AJ277743	Fagus sylvatica	protein phpsphatase 2C (PP2C). pp2C1. ABA-induced protein.
CAC10358.1	AJ277086	Nicotiana tabacum	protein phosphatase 2C. PP2C1.
CAC10359.1	AJ277087	Nicotiana tabacum	protein phosphatase 2C. PP2C2.
AAC36700.1	AF075582	Mesembryanthemum crystallinum	protein phosphatase-2C. PP2C.
CAC09575.1	AJ298987	Fagus sylvatica	protein phosphatase 2C (PP2C). pp2Cf1.
AAK20060.1	AC025783	Oryza sativa	putative protein phosphatase 2C. OSJNBa0001O14.1.
CAB90634.1	AJ277744	Fagus sylvatica	protein phosphatase 2C (PP2C). pp2C2. ABA and calcium induced protein.
AAC35951.1	AF079355	Mesembryanthemum crystallinum	protein phosphatase-2c. PP2C.
AAD11430.1	AF097667	Mesembryanthemum crystallinum	protein phosphatase 2C homolog. PP2C.
AAB93832.1	U81960	Zea mays	kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases; type 2C protein phosphatase. kinase associated protein phosphatase. KAPP.
AAC26828.1	AF075603	Oryza sativa	kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases. kinase associated protein phosphatase. kapp. type 2C protein phosphatase.
AAC36699.1	AF075581	Mesembryanthemum crystallinum	protein phosphatase-2C. PP2C.
CAC09576.1	AJ298988	Fagus sylvatica	protein phosphatase 2C (PP2C). pp2Cf2.
SEQ ID NO: 777			
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrkl.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.

CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.

BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAB39435.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.2.
BAB07904.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.12.
BAA94518.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAF91324.1	AF244890	Glycine max	receptor-like protein kinase 3. RLK3. GmRLK3.
BAA82556.1	AB030083	Populus nigra	lectin-like protein kinase. PnLPK.
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.
SEQ ID NO: 779			
AAK31284.1	AC079890	Oryza sativa	putative quinone oxidoreductase. OSJNBb0089A17.10.
BAA78050.1	AB027757	Cicer arietinum	NADPH oxidoreductase homolog.
BAA83082.1	AB030704	Lithospermum erythrorhizon	LEDI-4 protein. LEDI-4. preferentially expressed in darkness; putative NADPH quinone oxidoreductase; similar to zeta-crystallin.
AAG53944.1	AF304461	Triphysaria versicolor	quinone-oxidoreductase QR1. TvQR1.
SEQ ID NO: 780			
AAK17067.1	AF254558	Oryza sativa	NAC6. NAC6.

BAA89800.1	AB028185	Oryza sativa	OsNAC6 protein. OsNAC6.
BAA89799.1	AB028184	Oryza sativa	OsNAC5 protein. OsNAC5.
BAA89798.1	AB028183	Oryza sativa	OsNAC4 protein. OsNAC4.
BAA89797.1	AB028182	Oryza sativa	OsNAC3 protein. OsNAC3.
BAA89801.1	AB028186	Oryza sativa	OsNAC7 protein. OsNAC7.
AAF68626.1	AF254124	Medicago truncatula	NAC1. NAC1. NAC domain containing protein.
BAA89802.1	AB028187	Oryza sativa	OsNAC8 protein. OsNAC8.
BAA78417.1	AB021178	Nicotiana tabacum	NAC-domain protein. TERN. elicitor-responsive gene.
SEQ ID NO: 783			
CAA54390.1	X77134	Brassica napus	acyl-CoA binding protein.
CAA70200.1	Y08996	Ricinus communis	acyl-CoA-binding protein.
CAB56693.1	AJ249833	Digitalis lanata	binds medium- and long-chain acyl-coa esters. Acyl-CoA binding protein (ACBP). acbp3.
CAB56694.1	AJ249834	Digitalis lanata	binds medium- and long-chain acyl-coa esters. Acyl-CoA binding protein (ACBP). acbp4.
AAB67736.1	U35015	Gossypium hirsutum	acyl-CoA-binding protein.
AAB86851.1	AF031541	Fritillaria agrestis	acyl-CoA-binding protein. acabp.
SEQ ID NO: 784			
CAA58994.1	X84208	Sinapis alba	trypsin inhibitor 2. mti-2.
CAA76116.1	Y16190	Sinapis alba	trypsin inhibitor 2. mti-2.
SEQ ID NO: 785			
AAF66242.1	AF243180	Lycopersicon esculentum	dicyanin. binuclear blue copper protein; contains two stellacyanins linked together.

AAC32421.1	U65511	Cucumis sativus	putative oxygen activation and/or lignin formation. stellacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytocyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Stellacyanins; similar to Rhus vernicifera stellacyanin: SwissProt Accession Number P00302; similar to umecyanin: SwissProt Accession Number P42849; similar to mavicyanin; SwissProt Accession Number P80728; similar to BCB encoded by GenBank Accession Number Z15058; similar to F18A8.9, encoded by GenBank Accession Number AC003105; similar to F7F1.27 encoded by GenBank Accession Number AC004669; similar to F9D12.16 encoded by GenBank Accession Number AF077407; glycoprotein.
CAA80963.1	Z25471	Pisum sativum	blue copper protein.
AAD10251.1	AF031195	Triticum aestivum	blue copper-binding protein homolog. S85.
AAC64163.1	AF093537	Zea mays	blue copper protein. similar to pea blue copper protein in GenBank Accession Number Z25471.
CAA10134.1	AJ012693	Cicer arietinum	basic blue copper protein.
AAF66243.1	AF243181	Lycopersicon esculentum	plantacyanin. naturally occurring cupredoxin with a Val residue in the position of the axial ligand Met; member of the plantacyanin subfamily of a strictly plant-specific family of mononuclear blue copper proteins known as phytocyanins.
CAB65280.1	AJ248323	Medicago sativa subsp. x varia	basic blue protein. babl.
AAC32448.1	U76296	Spinacia oleracea	plantacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytocyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Plantacyanins; non-glycosylated.
SEQ ID NO: 793			
BAA81862.1	AB026295	Oryza sativa	Similar to leucoanthocyanidin dioxygenase.(AJ440611).
AAB39995.1	U82432	Dianthus caryophyllus	anthocyanidin synthase. allele: S; 2-oxoglutarat-dependent dioxygenase.
BAA36554.1	AB011796	Citrus unshiu	flavonol synthase. CitFLS.
AAD56580.1	AF184273	Daucus carota	leucoanthocyanidin dioxygenase 1. LDOX1. 2-oxoglutarate dependent dioxygenase.
AAD56581.1	AF184274	Daucus carota	leucoanthocyanidin dioxygenase 2. LDOX. 2-oxoglutarate dependent dioxygenase.
CAA50498.1	X71360	Malus sp.	anthocyanidin hydroxylase. apple equivalent to 'Candi' from Antirrhinum majus.

AAD26205.1	AF117269	Malus x domestica	anthocyanidin synthase. ANS.
AAB82287.1	AF026058	Matthiola incana	anthocyanidin synthase.
CAA80264.1	Z22543	Petunia x hybrida	flavonol synthase.
AAF64168.1	AF240764	Eustoma grandiflorum	flavonol synthase. fls.
BAA20143.1	AB003779	Perilla frutescens	leucoanthocyanidin dioxygenase.
AAB66560.1	AF015885	Callistephus chinensis	anthocyanidin synthase.
BAB21477.1	AB044091	Torenia fournieri	anthocyanidin synthase. 2-oxoglutarate dependent oxygenase.
CAA63092.1	X92178	Solanum tuberosum	flavonol synthase.
AAD26261.1	AF119095	Malus x domestica	flavonol synthase. FLS.
CAA53580.1	X75966	Vitis vinifera	leucoanthocyanidin dioxygenase. LDOX.
BAA75305.1	AB023786	Ipomoea batatas	anthocyanidin synthase. ans I.
AAB84049.1	AF028602	Ipomoea purpurea	anthocyanidin synthase. ANS-FL1.
BAA75306.1	AB023787	Ipomoea batatas	anthocyanidin synthase. ans II.
CAA73094.1	Y12489	Forsythia x intermedia	anthocyanidin synthase.
CAA69252.1	Y07955	Oryza sativa	anthocyanidin synthase. ANS.
SEQ ID NO: 794			
AAD10204.1	AF030260	Vicia sativa	CYP94A1. vagh111. cytochrome P450 fatty acid hydroxylase; Method: conceptual translation with partial peptide sequencing.
AAG33645.1	AF092917	Vicia sativa	cytochrome P450-dependent fatty acid hydroxylase. CYP94A2.
AAG17470.1	AF123609	Triticum aestivum	cytochrome P450.
BAA99523.1	AP002484	Oryza sativa	putative cytochrome P450. P0489A01.14.
AAK31592.1	AY029178	Brassica rapa subsp. pekinensis	cytochrome P450. mf-CYP450. possible relevance to male-sterility.

BAA99522.1	AP002484	Oryza sativa	putative cytochrome P450. P0489A01.13.
BAA83370.1	AP000391	Oryza sativa	ESTs AU056036(S20239),C72753(E2173), AU056035(S20239) correspond to a region of the predicted gene.; Similar to putative cytochrome P-450 (AC003680).
CAB41474.1	AJ238402	Catharanthus roseus	cytochrome P450. CYP96C1.
AAB94586.1	AF022457	Glycine max	CYP97B2p. CYP97B2. cytochrome P450 monooxygenase.
AAK20054.1	AC025783	Oryza sativa	putative cytochrome P450 monooxygenase. OSJNBa0001O14.16.
AAK38086.1	AF321862	Lolium rigidum	putative cytochrome P450.
AAK38085.1	AF321861	Lolium rigidum	putative cytochrome P450.
AAB94588.1	AF022459	Glycine max	CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
CAA89260.1	Z49263	Pisum sativum	cytochrome P450.
AAG09208.1	AF175278	Pisum sativum	wound-inducible P450 hydroxylase. CYP82A1.
AAC49188.2	U29333	Pisum sativum	cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
BAB19083.1	AP002744	Oryza sativa	putative cytochrome P450. P0006C01.25. contains ESTs AU081507(C12518),C26520(C12518).
BAB19104.1	AP002839	Oryza sativa	putative cytochrome P450. P0688A04.10. contains ESTs AU081507(C12518),C26520(C12518).
AAK38092.1	AF321868	Lolium rigidum	putative cytochrome P450.
CAA04117.1	AJ000478	Helianthus tuberosus	fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'-race).
AAK38091.1	AF321867	Lolium rigidum	putative cytochrome P450.
CAA04116.1	AJ000477	Helianthus tuberosus	fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
BAA22423.1	AB001380	Glycyrrhiza echinata	cytochrome P450. CYP93B1.
CAA71876.1	Y10982	Glycine max	putative cytochrome P450.



BAB39252.1	AP002968	Oryza sativa	putative cytochrome P450. P0416G11.1.
AAA33106.1	L10081	Catharanthus roseus	cytochrome P-450 protein. CYP72. putative; CYP72 protein.
AAA17746.1	L19075	Catharanthus roseus	cytochrome P450. CYP72C. putative.
BAA74466.1	AB022733	Glycyrrhiza echinata	cytochrome P450. CYP Ge-51.
BAB19121.1	AP002839	Oryza sativa	putative cytochrome P450. P0688A04.28.
AAA17732.1	L19074	Catharanthus roseus	cytochrome P450. CYP72B.
BAA93634.1	AB025016	Lotus japonicus	cytochrome P450.
AAB05376.3	U35226	Nicotiana plumbaginifolia	putative cytochrome P-450.
AAB61965.1	U48435	Solanum chacoense	putative cytochrome P450.
AAF27282.1	AF122821	Capsicum annuum	cytochrome P450. PepCYP.
CAB50768.1	AJ243804	Cicer arietinum	putative isoflavone synthase. cytochrome P450. cyp93C3.
AAC34853.1	AF082028	Hemerocallis hybrid cultivar	putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3. mRNA accumulates in senescing petals.
CAB43505.1	AJ239051	Cicer arietinum	cytochrome P450. cyp81E2.
BAB21156.1	AP002899	Oryza sativa	putative cytochrome P450. P0456A01.12.
CAA50648.1	X71657	Solanum melongena	P450 hydroxylase.
BAB19112.1	AP002839	Oryza sativa	putative cytochrome P450. P0688A04.18. contains ESTs AU067870(C10320),AU067869(C10320).
BAB19091.1	AP002744	Oryza sativa	putative cytochrome P450. P0006C01.33. contains ESTs AU067870(C10320),AU067869(C10320).
BAA84072.1	AB028152	Torenia hybrida	flavone synthase II. cytochrome P450. TFNS5.
BAA76380.1	AB023636	Glycyrrhiza echinata	cytochrome P450. CYP Ge-8.
CAA72208.1	Y11404	Zea mays	cytochrome p450. cyp71c2.

CAA57423.1	X81829	<i>Zea mays</i>	cytochrome P450. CYP71C2. family CYP71, subfamily CYP71C.
BAB12433.1	AB025030	<i>Coptis japonica</i>	p450.
SEQ ID NO: 798			
BAB21205.1	AP002913	<i>Oryza sativa</i>	nucleoid DNA-binding protein cnd41-like protein. P0480E02.11. contains ESTs AU166073(E31027),AU029516(E31027).
BAA22813.1	D26015	<i>Nicotiana tabacum</i>	aspartic protease activity. CND41, chloroplast nucleoid DNA binding protein. cnd41.
SEQ ID NO: 804			
AAD46491.1	AF135014	<i>Zea mays</i>	dihydrolipoamide S-acetyltransferase. pyruvate dehydrogenase complex E2 subunit.
SEQ ID NO: 805			
BAA85412.1	AP000615	<i>Oryza sativa</i>	ESTs AU065232(E60855),C23624(S1554), AU078241(E60855) correspond to a region of the predicted gene.; similar to putative adenylate kinase. (AC005896).
BAA01181.1	D10335	<i>Oryza sativa</i>	adenylate kinase-b. Adk-b.
BAA01180.1	D10334	<i>Oryza sativa</i>	adenylate kinase-a. Adk-a.
BAA94761.1	AB041773	<i>Oryza sativa</i>	adenylate kinase. Adk-a.
AAB68604.1	U82330	<i>Prunus armeniaca</i>	adenylate kinase homolog.
AAF23372.1	AF187063	<i>Oryza sativa</i>	catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase b. ura6.
AAF23371.1	AF187062	<i>Oryza sativa</i>	catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase a. ura6.
AAD41679.1	AF086603	<i>Ceratopteris richardii</i>	adenylate kinase. ADK1.
BAA85443.1	AP000616	<i>Oryza sativa</i>	similar to UMP/CMP kinase (AF000147).
SEQ ID NO: 808			
CAA41774.1	X59046	<i>Oryza sativa</i>	sucrose-UDP glucosyltransferase (isoenzyme 2). RSs2.
BAA89049.1	AB029401	<i>Citrus unshiu</i>	sucrose synthase. CitSUS1-2.
AAA34196.1	L19762	<i>Lycopersicon esculentum</i>	sucrose synthase.

BAA88905.1	AB022092	Citrus unshiu
sucrose synthase. CitSUS1.		
AAD28641.1	U73588	Gossypium hirsutum
sucrose synthase.		
CAA49428.1	X69773	Vicia faba
sucrose synthase. VfSucs.		
AAC37346.1	M97551	Vicia faba
cleavage of sucrose. UDP-glucose:D-fructose-2-glucosyltransferase. putative.		
CAA09681.1	AJ011535	Lycopersicon esculentum
sucrose synthase. sus2.		
AAA97572.1	U24088	Solanum tuberosum
sucrose synthase.		
CAA09593.1	AJ011319	Lycopersicon esculentum
sucrose synthase. sus3.		
CAB40794.1	AJ131943	Medicago truncatula
sucrose synthase. sucS1.		
AAC17867.1	AF049487	Medicago sativa
sucrose hydrolysis. sucrose synthase.		
CAB40795.1	AJ131964	Medicago truncatula
sucrose synthase. sucS1.		
CAA65640.1	X96939	Tulipa gesneriana
sucrose-synthase 21.		
AAA97571.1	U24087	Solanum tuberosum
sucrose synthase.		
CAA63122.1	X92378	Alnus glutinosa
sucrose synthase. sus1.		
AAA33514.1	L22296	Zea mays
UDP-glucose:D-fructose 2-glucosyl-transferase. Sus1.		
CAA65639.1	X96938	Tulipa gesneriana
sucrose-synthase 1.		
AAC41682.1	L03366	Oryza sativa
sucrose synthase 3. RSs3.		
CAA75793.1	Y15802	Hordeum vulgare
sucrose synthase 2. Ss2.		
CAA49551.1	X69931	Hordeum vulgare
sucrose synthase. Ss2.		
CAA76056.1	Y16090	Daucus carota
sucrose synthase isoform I. Susy*Dcl.		
CAA53081.1	X75332	Daucus carota
sucrose synthase.		
AAA33515.1	L33244	Zea mays
sucrose synthase 2. Sus1.		

BAB20799.1	AB045710	Pyrus pyrifolia	sucrose synthase 1. PypSUS1.
CAA03935.1	AJ000153	Triticum aestivum	sucrose synthase type 2.
AAC39323.1	AF030231	Glycine max	sucrose synthase. SS. nodulin-100.
BAA01108.1	D10266	Vigna radiata	sucrose synthase. vss1.
CAA09910.1	AJ012080	Pisum sativum	sucrose synthase.
AAC28107.1	AF079851	Pisum sativum	nodule-enhanced sucrose synthase. ness.
CAC32462.1	AJ311496	Pisum sativum	sucrose metabolism. sucrose synthase isoform 3. sus3.
CAA57881.1	X82504	Chenopodium rubrum	sucrose synthase. CSS1.
CAA26229.1	X02382	Zea mays	sucrose synthase.
CAA26247.1	X02400	Zea mays	sucrose synthase.
CAA46017.1	X64770	Oryza sativa	sucrose synthase. RSs1.
CAB38022.1	AJ132000	Craterostigma plantagineum	sucrose metabolism. sucrose synthase. Ss2.
CAA78747.1	Z15028	Oryza sativa	sucrose synthase.
AAF85966.1	AF263384	Saccharum officinarum	sucrose synthase-1.
CAA46701.1	X65871	Hordeum vulgare	sucrose synthase.
CAA04543.1	AJ001117	Triticum aestivum	sucrose synthase type I. Ss1.
BAA88904.1	AB022091	Citrus unshiu	sucrose synthase. CitSUSA.
BAA88981.1	AB025778	Citrus unshiu	sucrose synthase. CitSUSA-2.
CAA04512.1	AJ001071	Pisum sativum	second sucrose synthase.
CAA76057.1	Y16091	Daucus carota	sucrose synthase isoform II. Susy*Dc2.
CAB38021.1	AJ131999	Craterostigma plantagineum	sucrose metabolism. sucrose synthase. Ss1.

CAA57499.1	X81974	Beta vulgaris	sucrose synthase. SBSS1.
CAA47264.1	X66728	Hordeum vulgare	sucrose synthase.
SEQ ID NO: 809			
AAB69317.1	AF012861	Petroselinum crispum	plastidic glucose-6-phosphate dehydrogenase. pG6PDH.
AAF87216.1	AF231351	Nicotiana tabacum	plastidic glucose 6-phosphate dehydrogenase. G6PDHP2.
CAA67782.1	X99405	Nicotiana tabacum	glucose-6-phosphate dehydrogenase. G6PD.
CAB52708.1	AJ010712	Solanum tuberosum	glucose-6-phosphate 1-dehydrogenase. g6pd.
CAB52685.1	AJ132346	Dunaliella bioculata	plastidic glucose-6-phosphate dehydrogenase. g6PD.
CAA58775.1	X83923	Solanum tuberosum	glucose-6-phosphate dehydrogenase.
CAA03941.1	AJ000184	Spinacia oleracea	Glucose-6-phosphate dehydrogenase. G6PD.
CAA03939.1	AJ000182	Spinacia oleracea	Glucose-6-phosphate dehydrogenase. G6PD.
CAA04994.1	AJ001772	Nicotiana tabacum	glucose-6-phosphate dehydrogenase. TCG18.
CAA03940.1	AJ000183	Spinacia oleracea	Glucose-6-phosphate dehydrogenase. G6PD.
AAD11426.1	AF097663	Mesembryanthemum crystallinum	cytoplasmic glucose-6-phosphate 1-dehydrogenase. G6PD.
AAB41552.1	U18238	Medicago sativa subsp. sativa	glucose-6-phosphate dehydrogenase.
CAA52442.1	X74421	Solanum tuberosum	glucose-6-phosphate 1-dehydrogenase. g6pdh. homotetramer.
AAB69318.1	AF012862	Petroselinum crispum	cytosolic glucose-6-phosphate dehydrogenase 1. cG6PDH1.
AAB69319.1	AF012863	Petroselinum crispum	cytosolic glucose-6-phosphate dehydrogenase 2. cG6PDH2.
CAA04992.1	AJ001769	Nicotiana tabacum	glucose-6-phosphate dehydrogenase. TCG6.
CAA04993.1	AJ001770	Nicotiana tabacum	glucose-6-phosphate dehydrogenase. TCG9.
BAA97662.1	AB029454	Triticum aestivum	glucose-6-phosphate dehydrogenase. g6pdh.

BAA97663.1	AB029455	Triticum aestivum	glucose-6-phosphate dehydrogenase. g6pdh.
BAA97664.1	AB029456	Triticum aestivum	glucose-6-phosphate dehydrogenase. g6pdh.
AAG23802.1	AF260736	Cucurbita pepo	plastidic glucose-6-phosphate dehydrogenase.
CAB66330.1	AJ279688	Betula pendula	glucose-6-phosphate dehydrogenase. g6pd.
BAA82155.1	AB011441	Triticum aestivum	glucose-6-phosphate dehydrogenase. WESR5. salt-stress responding gene.
CAA06200.1	AJ004900	Glycine max	pentose phosphate pathway oxidoreductase generating NADPH. glucose-6-phosphate-dehydrogenase.
SEQ ID NO: 812			
BAA08910.1	D50407	Cucumis sativus	glutamyl-tRNA reductase. hemA.
AAD16897.1	AF105221	Glycine max	converts glutamyl-tRNA to glutamate 1-semialdehyde. glutamyl-tRNA reductase precursor. gtr1.
BAA11091.1	D67088	Cucumis sativus	glutamyl-tRNA reductase. hemA2.
BAA25003.1	AB011416	Oryza sativa	glutamyl-tRNA reductase.
AAG13620.1	AC078840	Oryza sativa	putative glutamyl-tRNA reductase. OSJNBb0073N24.1.
CAA60054.1	X86101	Hordeum vulgare	aminolevulinate synthesis (chlorophyll synthesis). glutamyl tRNA reductase. hemA 1. 1st isoform.
CAA63140.1	X92403	Hordeum vulgare	glutamyl-tRNA reductase. hemA1. isoform I.
BAA25167.1	D88382	Hordeum vulgare	glutamyl-tRNA reductase. hemA1. isoform 1.
CAA60055.1	X86102	Hordeum vulgare	aminolevulinate synthesis (chlorophyll synthesis). glutamyl tRNA reductase. hemA 2. 2nd isoform.
BAA25168.1	D88383	Hordeum vulgare	glutamyl-tRNA reductase. hemA3. isoform 3.
AAG41962.1	AF305613	Chlamydomonas reinhardtii	glutamyl-tRNA reductase precursor. HemA. pGtr.
AAG02480.1	AF294753	Hordeum vulgare	converts glutamyl-tRNA to glutamate 1-semialdehyde in the chlorophyll biosynthetic pathway. glutamyl-tRNA reductase. hemA2.

AAG02479.1	AF294752	Hordeum vulgare	converts glutamyl-tRNA to glutamate 1-semialdehyde in the chlorophyll biosynthetic pathway. glutamyl-tRNA reductase. hemA1.
SEQ ID NO: 813			
BAA82556.1	AB030083	Populus nigra	lectin-like protein kinase. PnLPK.
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
AAF43408.1	AF230515	Oryza sativa subsp. japonica	serine/threonine protein kinase. YK35.
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
BAB19337.1	AP003044	Oryza sativa	putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAA92953.1	AP001551	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).
BAB07906.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.14.
BAA94516.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrkl.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.

BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
AAD46420.1	AF100771	Hordeum vulgare	receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
AAD38286.1	AC007789	Oryza sativa	putative protein kinase. OSJNBa0049B20.13.
BAB40081.1	AP003074	Oryza sativa	putative receptor protein kinase. OSJNBa0004G10.30.
BAB18321.1	AP002865	Oryza sativa	putative receptor protein kinase. P0034C11.11.
BAA94517.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
BAA94529.2	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.



BAA94528.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
AAB47421.1	U59316	Lycopersicon esculentum	serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.

## SEQ ID NO: 814

AAF23903.1	AF194416	Oryza sativa	MAP kinase homolog. MAPK2. RMAPK2.
AAD52659.1	AF177392	Oryza sativa	blast and wounding induced mitogen-activated protein kinase. BWMK1. BWMK1 MAP kinase.
AAF23902.1	AF194415	Oryza sativa	MAP kinase homolog. MAPK1. RMAPK1.
AAD28617.1	AF129087	Medicago sativa	mitogen-activated protein kinase homologue. TDY1.
CAB61750.1	AJ275316	Cicer arietinum	MAP kinase protein.
AAB57843.1	U96716	Selaginella lepidophylla	MAP kinase-like protein. sdhn-6r.
AAF65766.1	AF242308	Euphorbia esula	mitogen-activated protein kinase. regulated by tyrosine and threonine phosphorylation.
BAB18271.1	AB035141	Chlamydomonas reinhardtii	mitogen-activated protein kinase. CrMPK2.
CAA58761.1	X83880	Nicotiana tabacum	p45Ntf4 serine/threonine protein kinase. ntf4.
CAA47099.1	X66469	Medicago sativa	MAP Kinase. MSK7.

AAB41548.1	L07042	Medicago sativa	autophosphorylating serine/threonine protein kinase. MAP kinase. MsERK1.
AAB58396.1	U94192	Nicotiana tabacum	salicylic acid-activated MAP kinase. NtSIPK.
CAA50036.1	X70703	Pisum sativum	MAP kinase homologue. PSMAPKIN.
AAF73236.1	AF153061	Pisum sativum	MAP kinase 3. Mapk3. PsMAPK3.
BAB32406.1	AB055515	Nicotiana tabacum	NRK1 MAPK. nrk1. A tobacco MAPK that is phosphorylated and activated by NQK1.
CAA58760.1	X83879	Nicotiana tabacum	p43Nft6 serine/threonine protein kinase. ntf6.
CAA57721.1	X82270	Medicago sativa	protein kinase. MMK4.
AAF81420.1	AF247136	Capsicum annuum	MAP kinase 2. MK2. CAMK2; wound, UV-C, and cold-inducible expression.
AAD37790.1	AF149424	Ipomoea batatas	MAP kinase.
AAG40580.1	AF216316	Oryza sativa	MAP kinase 2. protein kinase; MAP2.
CAB37188.1	AJ224336	Medicago sativa	MAP kinase. MMK3.
AAF61238.1	AF241166	Oryza sativa	MAP kinase MAPK2.
AAG40581.1	AF216317	Oryza sativa	MAP kinase 3. protein kinase; MAP3.
CAB61889.1	AJ251330	Oryza sativa	protein kinase. MAPK4 protein. mapk4.
CAA73323.1	Y12785	Petroselinum crispum	MAP kinase I.
CAC13967.1	AJ250311	Oryza sativa	protein kinase. MAPK2 protein. mapk2.
CAA56314.1	X79993	Avena sativa	MAP KINASE. Asmap1.
CAA49592.1	X69971	Nicotiana tabacum	serine/threonine protein kinase. NTF3.
CAA58466.1	X83440	Petunia x hybrida	MAP/ERK kinase 1. MEK1.
AAK01710.1	AF332873	Oryza sativa	MAP kinase BIMK1.
AAG40579.1	AF216315	Oryza sativa	MAP kinase 1. protein kinase; MAP1.

CAA57719.1	X82268	Medicago sativa	protein kinase. MMK2.
AAC28850.1	AF079318	Triticum aestivum	protein kinase. MAP kinase homolog. WCK-1.
AAD32204.1	AF134730	Prunus armeniaca	putative mitogen-activated protein kinase MAPK. MAP kinase.
BAA74734.1	AB016802	Zea mays	MAP kinase 5. ZmMPK5.
AAF73257.1	AF154329	Pisum sativum	MAP kinase PsMAPK2. Mapk2.
BAA09600.1	D61377	Nicotiana tabacum	WIPK. MAP (mitogen-activated protein) kinase.
AAF81419.1	AF247135	Capsicum annuum	MAP kinase 1. MK1. wound and UV-C inducible expression.
BAA74733.1	AB016801	Zea mays	MAP kinase 4. ZmMPK4.
CAA05328.1	AJ002314	Nicotiana tabacum	serine/threonine protein kinase. shaggy-like kinase 111. NSK 111.
CAA05329.1	AJ002315	Nicotiana tabacum	shaggy-like kinase 59. NSK 59.
CAA11861.1	AJ224164	Petunia x hybrida	shaggy kinase 6. PSK6.
CAA58595.1	X83620	Petunia x hybrida	Petunia Shaggy kinase 6. PSK6.
CAA11862.1	AJ224165	Petunia x hybrida	shaggy kinase 7. PSK7.
CAA58594.1	X83619	Petunia x hybrida	Petunia Shaggy kinase 4. PSK4.
AAA92823.1	U18365	Brassica napus	cyclin dependent protein kinase homolog; similar to moth bean p34cdc2 protein, PIR Accession Number JQ2243.
BAA92214.1	AP001278	Oryza sativa	ESTs C22403(C50132),C22404(C50132) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana shaggy related protein kinase ASK-gamma. (P43289).
CAA67554.1	X99100	Trifolium repens	protein kinase. trK.
SEQ ID NO: 816			
CAA65065.1	X95759	Solanum tuberosum	glycogen (starch) synthase.
CAA64173.1	X94400	Solanum tuberosum	soluble-starch-synthase. SSSIII.

AAC14014.1	AF023159	<i>Zea mays</i> starch synthase DULL1. dull1. similar to potato starch synthase SSIII; likely to be the maize starch synthase defined biochemically as SSII.
CAB40374.1	AJ225088	<i>Vigna unguiculata</i> ADP-glucose-starch glucosyltransferase. Starch synthase isoform SS III.
AAF88000.1	AF258609	<i>Aegilops tauschii</i> starch synthase III.
AAF87999.1	AF258608	<i>Triticum aestivum</i> starch synthase III. wSSIII.
CAB40375.1	AJ006752	<i>Vigna unguiculata</i> ADP-glucose starch glucosyltransferase. starch synthase, isoform V.
AAC14015.1	AF023160	<i>Zea mays</i> starch synthase DULL1. dull1. similar to potato starch synthase SSIII; like to be the maize starch synthase defined biochemically as SSII.
AAC17971.2	AF026422	<i>Chlamydomonas reinhardtii</i> soluble starch synthase. ADP-glucose:alpha-1, 4-D-glucan-4-alpha-D-glucosyltransferase.
AAD13342.1	AF019297	<i>Zea mays</i> starch synthase isoform zSTSII-2. zSSIIb.
CAB86618.1	AJ269502	<i>Triticum aestivum</i> transfers the glucosyl unit of ADP glucose to the non-reducing end of an alpha 1,4. starch synthase IIa-1. wSs2a-1.
CAA61269.1	X88790	<i>Pisum sativum</i> glycogen (starch) synthase.
CAB96626.1	AJ269503	<i>Triticum aestivum</i> transfers the glucosyl unit of ADP glucose to the non-reducing end of an alpha 1,4. starch synthase IIa-2. wSs2a-2.
CAB96627.1	AJ269504	<i>Triticum aestivum</i> transfers the glucosyl unit of ADP glucose to the non-reducing end of an alpha 1,4. starch synthase IIa-3. wSs2a-3.
CAA71442.1	Y10416	<i>Solanum tuberosum</i> soluble starch (bacterial glycogen) synthase. SS I.
AAD53263.1	AF155217	<i>Triticum aestivum</i> starch synthase IIA.
AAF37876.1	AF234163	<i>Hordeum vulgare</i> starch synthase I. SSI.
CAB99209.1	AJ292521	<i>Triticum aestivum</i> essential for starch synthesis. starch synthase I-1. wSsI-1.
AAD54661.1	AF091803	<i>Triticum aestivum</i> starch synthase I.
AAB17085.1	U66377	<i>Triticum aestivum</i> starch synthase. TaSS. EC 2.4.1.11.
CAB99210.1	AJ292522	<i>Triticum aestivum</i> essential for starch synthesis. starch synthase I-2. wSsI-2.

AAF03557.1	AF091802	<i>Aegilops tauschii</i> starch synthase I.
AAD13341.1	AF019296	<i>Zea mays</i> starch synthase isoform zSTSII-1. zSSIIa.
AAC17969.2	AF026420	<i>Chlamydomonas reinhardtii</i> ADP-Glucose:alpha-1, 4-D-glucan-4-alpha-D-glucosyltransferase. granule-bound starch synthase I precursor. STA2. GBSSI.
BAA82346.1	AB029546	<i>Phaseolus vulgaris</i> granule-bound starch synthase I. GBSSI.
CAA37732.1	X53694	<i>Oryza sativa</i> starch synthase.
CAA52273.1	X74160	<i>Manihot esculenta</i> starch (bacterial glycogen) synthase. GBSS.
AAF72561.1	AF141954	<i>Oryza sativa</i> granule-bound starch synthase. Waxy.
CAA46294.1	X65183	<i>Oryza sativa</i> glycogen (starch) synthase. waxy gene. starch granule enzyme.
AAF72562.1	AF141955	<i>Oryza sativa</i> granule-bound starch synthase. Waxy.
CAA44065.1	X62134	<i>Oryza sativa</i> starch biosynthesis. starch (bacterial glycogen) synthase. Wx.
AAB02197.1	U48227	<i>Triticum aestivum</i> soluble starch synthase.
AAF13168.1	AF173900	<i>Manihot esculenta</i> granule bound starch synthase II precursor. GBSSII. MEGBSSII.
CAA45472.1	X64108	<i>Oryza sativa</i> starch granule-bound starch synthase. waxy.
AAC61675.2	AF031162	<i>Oryza sativa</i> granule-bound starch synthase. Waxy.
AAC70779.1	AF097922	<i>Astragalus membranaceus</i> granule-bound glycogen (starch) synthase. GBSS.
CAA06958.1	AJ006293	<i>Antirrhinum majus</i> granule-bound starch synthase. waxy.
AAC19119.1	AF068834	<i>Ipomoea batatas</i> starch synthase.
AAD49850.1	AF165890	<i>Oryza sativa</i> subsp. <i>japonica</i> soluble starch synthase.
BAA81848.1	AB026295	<i>Oryza sativa</i> ESTs AU075322(C11109),D22430(C11109) correspond to a region of the predicted gene.; Rice gene for soluble starch synthase (SSS1), complete cds (exon1-15).(D38221).
BAA03739.1	D16202	<i>Oryza sativa</i> soluble starch synthase precursor.

CAA61268.1	X88789	Pisum sativum glycogen (starch) synthase.
AAA86423.1	U44126	Ipomoea batatas starch synthase. SPSS67.
AAF14233.1	AF109395	Triticum aestivum granule-bound starch synthase GBSSII.
CAA41359.1	X58453	Solanum tuberosum glycogen (starch) synthase. amf. waxy protein, granule-bound starch synthase.
AAG43519.1	AF210699	Perilla frutescens granule-bound starch synthase. GBSSI. waxy protein.
SEQ ID NO: 819		
BAA13032.1	D86180	Pisum sativum phosphoribosylanthranilate transferase. PAT1.
SEQ ID NO: 822		
AAB86850.1	AF031540	Fritillaria agrestis cytochrome C. cytC.
AAC84135.1	AF101422	Cichorium intybus cytochrome.
BAA02159.1	D12634	Oryza sativa 'cytochrome C'.
AAA63515.1	M63704	Oryza sativa cytochrome c. Cc-1.
AAA92712.1	L77113	Helianthus annuus cytochrome c. cytcl. putative.
AAB70265.1	AF017367	Oryza sativa cytochrome C.
AAA33084.1	M35173	Chlamydomonas reinhardtii apocytochrome c (cyc).
CAB16954.1	Z99829	Chlamydomonas reinhardtii cytochrome c. CYC1.
CAA79708.1	Z21499	Stellaria longipes mitochondrial cytochrome c.
SEQ ID NO: 823		
BAA02159.1	D12634	Oryza sativa 'cytochrome C'.
AAA63515.1	M63704	Oryza sativa cytochrome c. Cc-1.
AAB86850.1	AF031540	Fritillaria agrestis cytochrome C. cytC.
AAC84135.1	AF101422	Cichorium intybus cytochrome.

AAA92712.1	L77113	Helianthus annuus	cytochrome c. cytcl. putative.
AAB70265.1	AF017367	Oryza sativa	cytochrome C.
AAA33084.1	M35173	Chlamydomonas reinhardtii	apocytochrome c (cyc).
CAB16954.1	Z99829	Chlamydomonas reinhardtii	cytochrome c. CYC1.
CAA79708.1	Z21499	Stellaria longipes	mitochondrial cytochrome c.
SEQ ID NO: 825			
BAB17113.1	AP002866	Oryza sativa	putative white protein; ATP-binding cassette transporter. P0410E01.34.
AAF43869.1	AF166114	Chloroplast Mesostigma viride	probable transport protein. cysA.
BAA90508.1	AP001111	Oryza sativa	similar to ABC transporter of Arabidopsis thaliana (AC004697).
AAD54843.1	AF137379	Chloroplast Nephroselmis olivacea	probable transport protein. cysA.
BAA57907.1	AB001684	Chlorella vulgaris	sulfate transport system permease protein. cysA.
BAA90507.1	AP001111	Oryza sativa	similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAB40032.1	AP003046	Oryza sativa	putative ABC transporter. P0445D12.3.
AAG49003.1	AY013246	Hordeum vulgare	putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and comparative sequence.
BAB21275.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.6.
AAG45492.1	AY013245	Oryza sativa	36I5.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and comparative sequence.
AAG49002.1	AY013246	Hordeum vulgare	putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative sequencing.
BAB21276.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
AAD10836.1	U52079	Solanum tuberosum	P-glycoprotein. pmdr1. binds ATP; ATPase; transporter; transmembrane protein.
BAB21279.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.10. contains ESTs AU065360(R3463), AU101680(R3463).

BAB21273.1 AP002844 *Oryza sativa*  
putative ABC transporter protein. P0410E03.4.

BAA83352.1 AP000391 *Oryza sativa*  
ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.;  
Similar to ABC transporter-7 (U43892).

BAA96612.1 AP002482 *Oryza sativa*  
Similar to *Arabidopsis thaliana* chromosome 2, BAC F14M4 ; putative ABC transporter  
(AC004411).

## SEQ ID NO: 827

AAG34803.1 AF243368 *Glycine max*  
glutathione S-transferase GST 13.

AAG16758.1 AY007560 *Lycopersicon esculentum*  
putative glutathione S-transferase T3.

AAG34798.1 AF243363 *Glycine max*  
glutathione S-transferase GST 8.

AAF64450.1 AF239928 *Euphorbia esula*  
glutathione S-transferase. similar to auxin-inducible GST.

AAG34807.1 AF243372 *Glycine max*  
glutathione S-transferase GST 17.

AAG34796.1 AF243361 *Glycine max*  
glutathione S-transferase GST 6.

AAG16759.1 AY007561 *Lycopersicon esculentum*  
putative glutathione S-transferase T4.

AAG34797.1 AF243362 *Glycine max*  
glutathione S-transferase GST 7.

AAG34801.1 AF243366 *Glycine max*  
glutathione S-transferase GST 11.

AAG34804.1 AF243369 *Glycine max*  
glutathione S-transferase GST 14.

AAG34809.1 AF243374 *Glycine max*  
glutathione S-transferase GST 19.

AAG34808.1 AF243373 *Glycine max*  
glutathione S-transferase GST 18.

AAG34810.1 AF243375 *Glycine max*  
glutathione S-transferase GST 20.

AAG16757.1 AY007559 *Lycopersicon esculentum*  
putative glutathione S-transferase T2.

AAG16756.1 AY007558 *Lycopersicon esculentum*  
putative glutathione S-transferase T1.

AAG34844.1 AF244701 *Zea mays*  
glutathione S-transferase GST 36.

AAG34805.1 AF243370 *Glycine max*  
glutathione S-transferase GST 15.



AAG34831.1	AF244688	Zea mays	glutathione S-transferase GST 23.
AAG34832.1	AF244689	Zea mays	glutathione S-transferase GST 24.
AAG34849.1	AF244706	Zea mays	glutathione S-transferase GST 41.
AAG34802.1	AF243367	Glycine max	glutathione S-transferase GST 12.
CAA09187.1	AJ010448	Alopecurus myosuroides	glutathione transferase. GST1a.
AAG34829.1	AF244686	Zea mays	glutathione S-transferase GST 21.
CAA09188.1	AJ010449	Alopecurus myosuroides	glutathione transferase. GST1b.
AAA68430.1	J03679	Solanum tuberosum	glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.
AAG34836.1	AF244693	Zea mays	glutathione S-transferase GST 28.
AAG34837.1	AF244694	Zea mays	glutathione S-transferase GST 29.
AAG34800.1	AF243365	Glycine max	glutathione S-transferase GST 10.
AAC18566.1	AF048978	Glycine max	2,4-D inducible glutathione S-transferase. GSTa.
AAC32118.1	AF051214	Picea mariana	probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAF22517.1	AF118924	Papaver somniferum	glutathione S-transferase 1. GST1.
AAF22518.1	AF118925	Papaver somniferum	glutathione S-transferase 2. GST2.
AAG32471.1	AF309378	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTU4.
AAG34806.1	AF243371	Glycine max	glutathione S-transferase GST 16.
CAA04391.1	AJ000923	Carica papaya	glutathione transferase. PGST1.
AAG32472.1	AF309379	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTU3.
AAG34833.1	AF244690	Zea mays	glutathione S-transferase GST 25.
CAA71784.1	Y10820	Glycine max	glutathione transferase.

AAG34847.1 AF244704 Zea mays  
glutathione S-transferase GST 39.

AAF22519.1 AF118926 Papaver somniferum  
glutathione S-transferase 3. GST3.

SEQ ID NO: 828

AAG34803.1 AF243368 Glycine max  
glutathione S-transferase GST 13.

AAG34797.1 AF243362 Glycine max  
glutathione S-transferase GST 7.

AAG34798.1 AF243363 Glycine max  
glutathione S-transferase GST 8.

AAF64450.1 AF239928 Euphorbia esula  
glutathione S-transferase. similar to auxin-inducible GST.

AAG16758.1 AY007560 Lycopersicon esculentum  
putative glutathione S-transferase T3.

AAG34796.1 AF243361 Glycine max  
glutathione S-transferase GST 6.

AAG16759.1 AY007561 Lycopersicon esculentum  
putative glutathione S-transferase T4.

AAG34801.1 AF243366 Glycine max  
glutathione S-transferase GST 11.

AAG34804.1 AF243369 Glycine max  
glutathione S-transferase GST 14.

AAG34807.1 AF243372 Glycine max  
glutathione S-transferase GST 17.

AAG34809.1 AF243374 Glycine max  
glutathione S-transferase GST 19.

AAG34810.1 AF243375 Glycine max  
glutathione S-transferase GST 20.

AAG16757.1 AY007559 Lycopersicon esculentum  
putative glutathione S-transferase T2.

AAG16756.1 AY007558 Lycopersicon esculentum  
putative glutathione S-transferase T1.

AAG34802.1 AF243367 Glycine max  
glutathione S-transferase GST 12.

AAG34808.1 AF243373 Glycine max  
glutathione S-transferase GST 18.

AAG34844.1 AF244701 Zea mays  
glutathione S-transferase GST 36.

CAA09188.1 AJ010449 Alopecurus myosuroides  
glutathione transferase. GST1b.

CAA09187.1	AJ010448	<i>Alopecurus myosuroides</i> glutathione transferase. GST1a.
AAG32472.1	AF309379	<i>Oryza sativa</i> subsp. <i>japonica</i> putative glutathione S-transferase OsGSTU3.
AAA68430.1	J03679	<i>Solanum tuberosum</i> glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.
AAG34837.1	AF244694	<i>Zea mays</i> glutathione S-transferase GST 29.
AAG34800.1	AF243365	<i>Glycine max</i> glutathione S-transferase GST 10.
AAG34831.1	AF244688	<i>Zea mays</i> glutathione S-transferase GST 23.
AAC32118.1	AF051214	<i>Picea mariana</i> probable glutathione S-transferase. Sb18. similar to <i>Nicotiana tabacum</i> probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAG34805.1	AF243370	<i>Glycine max</i> glutathione S-transferase GST 15.
AAC18566.1	AF048978	<i>Glycine max</i> 2,4-D inducible glutathione S-transferase. GSTa.
AAG34829.1	AF244686	<i>Zea mays</i> glutathione S-transferase GST 21.
CAA04391.1	AJ000923	<i>Carica papaya</i> glutathione transferase. PGST1.
CAA71784.1	Y10820	<i>Glycine max</i> glutathione transferase.
AAG34795.1	AF243360	<i>Glycine max</i> glutathione S-transferase GST 5.
AAG34836.1	AF244693	<i>Zea mays</i> glutathione S-transferase GST 28.
AAG34832.1	AF244689	<i>Zea mays</i> glutathione S-transferase GST 24.
AAG34833.1	AF244690	<i>Zea mays</i> glutathione S-transferase GST 25.
AAG34849.1	AF244706	<i>Zea mays</i> glutathione S-transferase GST 41.
AAG34806.1	AF243371	<i>Glycine max</i> glutathione S-transferase GST 16.
CAA09189.1	AJ010450	<i>Alopecurus myosuroides</i> glutathione transferase. GST1c.
SEQ ID NO: 829		
AAG34803.1	AF243368	<i>Glycine max</i> glutathione S-transferase GST 13.

AAF64450.1 AF239928 *Euphorbia esula*  
glutathione S-transferase. similar to auxin-inducible GST.

AAG16758.1 AY007560 *Lycopersicon esculentum*  
putative glutathione S-transferase T3.

AAG34798.1 AF243363 *Glycine max*  
glutathione S-transferase GST 8.

AAG34801.1 AF243366 *Glycine max*  
glutathione S-transferase GST 11.

AAG34797.1 AF243362 *Glycine max*  
glutathione S-transferase GST 7.

AAG34796.1 AF243361 *Glycine max*  
glutathione S-transferase GST 6.

AAG34807.1 AF243372 *Glycine max*  
glutathione S-transferase GST 17.

AAG16759.1 AY007561 *Lycopersicon esculentum*  
putative glutathione S-transferase T4.

AAG34804.1 AF243369 *Glycine max*  
glutathione S-transferase GST 14.

AAG34810.1 AF243375 *Glycine max*  
glutathione S-transferase GST 20.

AAG34809.1 AF243374 *Glycine max*  
glutathione S-transferase GST 19.

AAG16757.1 AY007559 *Lycopersicon esculentum*  
putative glutathione S-transferase T2.

AAG16756.1 AY007558 *Lycopersicon esculentum*  
putative glutathione S-transferase T1.

AAG34805.1 AF243370 *Glycine max*  
glutathione S-transferase GST 15.

AAC18566.1 AF048978 *Glycine max*  
2,4-D inducible glutathione S-transferase. GSTa.

AAG34808.1 AF243373 *Glycine max*  
glutathione S-transferase GST 18.

AAG34800.1 AF243365 *Glycine max*  
glutathione S-transferase GST 10.

AAG34829.1 AF244686 *Zea mays*  
glutathione S-transferase GST 21.

AAG34802.1 AF243367 *Glycine max*  
glutathione S-transferase GST 12.

AAG34837.1 AF244694 *Zea mays*  
glutathione S-transferase GST 29.

CAA09187.1 AJ010448 *Alopecurus myosuroides*  
glutathione transferase. GST1a.

CAA09188.1	AJ010449	<i>Alopecurus myosuroides</i> glutathione transferase. GST1b.
AAG34849.1	AF244706	<i>Zea mays</i> glutathione S-transferase GST 41.
AAG34844.1	AF244701	<i>Zea mays</i> glutathione S-transferase GST 36.
AAG34806.1	AF243371	<i>Glycine max</i> glutathione S-transferase GST 16.
CAA71784.1	Y10820	<i>Glycine max</i> glutathione transferase.
AAA68430.1	J03679	<i>Solanum tuberosum</i> glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.
CAA04391.1	AJ000923	<i>Carica papaya</i> glutathione transferase. PGST1.
AAG34836.1	AF244693	<i>Zea mays</i> glutathione S-transferase GST 28.
AAG34831.1	AF244688	<i>Zea mays</i> glutathione S-transferase GST 23.
AAG34847.1	AF244704	<i>Zea mays</i> glutathione S-transferase GST 39.
AAC32118.1	AF051214	<i>Picea mariana</i> probable glutathione S-transferase. Sb18. similar to <i>Nicotiana tabacum</i> probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAF29773.1	AF159229	<i>Gossypium hirsutum</i> glutathione S-transferase. GST.
AAG32472.1	AF309379	<i>Oryza sativa</i> subsp. <i>japonica</i> putative glutathione S-transferase OsGSTU3.
AAG41204.1	AF321437	<i>Suaeda maritima</i> glutathione transferase.
CAC24549.1	AJ296343	<i>Cichorium intybus</i> x <i>Cichorium endivia</i> glutathione S-transferase. chi-GST1. auxin-induced GST.
SEQ ID NO: 830		
AAD37699.1	AF145730	<i>Oryza sativa</i> homeodomain leucine zipper protein. Oshox6. transcription factor.
BAA93461.1	AB028073	<i>Physcomitrella patens</i> homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.
AAF01765.1	AF184278	<i>Glycine max</i> homeodomain-leucine zipper protein 57. Hdl57. transcription factor.
AAF01764.2	AF184277	<i>Glycine max</i> homeodomain-leucine zipper protein 56. Hdl56. transcription factor.
BAA93466.1	AB028078	<i>Physcomitrella patens</i> homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.

CAB67118.1	Y17306	<i>Lycopersicon esculentum</i>	homeodomain protein. h52.
AAF73482.1	AF268422	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	hb-6-like protein. transcription factor; similar to <i>Arabidopsis thaliana</i> hb-6 protein.
AAD37697.1	AF145728	<i>Oryza sativa</i>	homeodomain leucine zipper protein. Oshox4. transcription factor.
BAA21017.1	D26578	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.
BAA05624.1	D26575	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.
BAA93460.1	AB028072	<i>Physcomitrella patens</i>	homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.
BAA93464.1	AB028076	<i>Physcomitrella patens</i>	homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.
BAA93467.1	AB028079	<i>Physcomitrella patens</i>	homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.
BAA93465.1	AB028077	<i>Physcomitrella patens</i>	homeobox protein PpHB6. PpHB6. homeodomain-leucine zipper gene.
BAA05625.1	D26576	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.
BAA93468.1	AB028080	<i>Physcomitrella patens</i>	homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.
BAA05623.1	D26574	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.
BAA05622.1	D26573	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.
AAD37698.1	AF145729	<i>Oryza sativa</i>	homeodomain leucine zipper protein. Oshox5. transcription factor.
CAA64221.1	X94449	<i>Pimpinella brachycarpa</i>	transcription activator. homeobox-leucine zipper protein. PHZ4.
CAA64152.1	X94375	<i>Pimpinella brachycarpa</i>	transcription activator. homeobox-leucine zipper protein.
CAA64491.1	X95193	<i>Pimpinella brachycarpa</i>	transcription activator. homeobox-leucine zipper protein.
BAA93463.1	AB028075	<i>Physcomitrella patens</i>	homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.
CAA06728.1	AJ005833	<i>Craterostigma plantagineum</i>	transcription factor. homeodomain leucine zipper protein. hb-2.

AAD37695.1	AF145726	Oryza sativa	homeodomain leucine zipper protein. Oshox2. transcription factor.
CAA65456.2	X96681	Oryza sativa	transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.
AAF19980.1	AF211193	Oryza sativa	homeodomain-leucine zipper transcription factor. Hox1. hox1.
AAK31270.1	AC079890	Oryza sativa	homeodomain leucine zipper protein hox1. OSJNBb0089A17.12.
CAA63222.1	X92489	Glycine max	transcription activator. homeobox-leucine zipper protein.
CAA06717.1	AJ005820	Craterostigma plantagineum	transcription factor. homeodomain leucine zipper protein. hb-1.
AAA79778.1	L48485	Helianthus annuus	homeodomain protein. putative.
SEQ ID NO: 831			
CAA06334.1	AJ005077	Lycopersicon esculentum	protein kinase. TCTR2 protein. TCTR2.
AAG31141.1	AF305911	Oryza sativa	EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAG31142.1	AF305912	Hordeum vulgare	EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAK30005.1	AY029067	Rosa hybrid cultivar	CTR2 protein kinase.
AAD46406.1	AF096250	Lycopersicon esculentum	ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.
CAA73722.1	Y13273	Lycopersicon esculentum	putative protein kinase.
AAD10057.1	AF110519	Lycopersicon esculentum	ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.
AAD10056.1	AF110518	Lycopersicon esculentum	ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.
AAA34002.1	M67449	Glycine max	protein kinase. PK6.
AAK11734.1	AY027437	Arachis hypogaea	serine/threonine/tyrosine kinase.
BAB16918.1	AP002863	Oryza sativa	putative protein kinase. P0005A05.22.
CAC09580.1	AJ298992	Fagus sylvatica	Abscisic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.

CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
AAF59906.1	AF197947	Glycine max	receptor protein kinase-like protein. CLV1B.
AAF59905.1	AF197946	Glycine max	receptor protein kinase-like protein. CLV1A.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
CAA08995.1	AJ010091	Brassica napus	MAP3K alpha 1 protein kinase. MAP3K alpha 1.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
CAA08997.1	AJ010093	Brassica napus	MAP3K beta 1 protein kinase. MAP3K beta 1.
CAB54520.1	AJ238845	Brassica napus	putative role in cell cycle control. MAP3K epsilon 1 protein kinase. MAP3Ke1.
AAF34436.1	AF172282	Oryza sativa	similar to mitogen-activated protein kinases. DUPR11.32.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
BAA06538.1	D31737	Nicotiana tabacum	protein-serine/threonine kinase.
AAF76189.1	AF271206	Rosa hybrid cultivar	CTR1-like protein kinase. Raf-like protein kinase.
BAA84787.1	AP000559	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).



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BAA83373.1 AP000391 *Oryza sativa*  
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

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AAF66615.1 AF142596 *Nicotiana tabacum*  
LRR receptor-like protein kinase.

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AAF91322.1 AF244888 *Glycine max*  
receptor-like protein kinase 1. RLK1. GmRLK1.

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AAD21872.1 AF078082 *Phaseolus vulgaris*  
receptor-like protein kinase homolog RK20-1.

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CAA61510.1 X89226 *Oryza sativa*  
leucine-rich repeat/receptor protein kinase. lrk2.

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BAA87853.1 AP000816 *Oryza sativa*  
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

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AAF91323.1 AF244889 *Glycine max*  
receptor-like protein kinase 2. RLK2. GmRLK2.

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AAF91324.1 AF244890 *Glycine max*  
receptor-like protein kinase 3. RLK3. GmRLK3.

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AAF43394.1 AF230501 *Oryza sativa* subsp. *japonica*  
serine/threonine protein kinase. YK1.

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AAK16409.1 AF320086 *Zea mays*  
serine threonine kinase 1. stk1. expressed in mature tassel.

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AAK21965.1 AY028699 *Brassica napus*  
receptor protein kinase PERK1.

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BAB39437.1 AP003338 *Oryza sativa*  
receptor-like kinase. OJ1212\_B09.6.

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AAK11568.1 AF318492 *Lycopersicon hirsutum*  
Pto-like protein kinase B. LhirPtoB.

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SEQ ID NO: 832

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AAF35901.1 AF230332 *Zinnia elegans*  
expansin 2.

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CAC19184.1 AJ291817 *Cicer arietinum*  
expansin.

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AAG13982.1 AF297521 *Prunus avium*  
expansin 1. Exp1. PruavExp1.

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BAB19676.1 AB029083 *Prunus persica*  
expansin. PchExp1.

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AAC33529.1 U93167 *Prunus armeniaca*  
expansin. PA-Exp1.

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AAC33530.1 AF038815 *Prunus armeniaca*  
expansin. Exp2.

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AAD47901.1 AF085330 *Pinus taeda*  
expansin.

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AAB37746.1	U30382	Cucumis sativus
expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.		
AAF21101.1	AF159563	Fragaria x ananassa
expansin. Exp2. ripening regulated.		
AAB40634.1	U64890	Pinus taeda
expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.		
AAB40637.1	U64893	Pinus taeda
expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.		
AAB40635.1	U64891	Pinus taeda
expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.		
CAB43197.1	AJ239068	Lycopersicon esculentum
cell wall loosening enzyme. expansin2. exp2.		
AAB40636.1	U64892	Pinus taeda
expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.		
AAC64201.1	AF096776	Lycopersicon esculentum
expansin. LeEXP2.		
AAD49956.1	AF167360	Rumex palustris
expansin. EXP1.		
AAC96081.1	AF049354	Nicotiana tabacum
involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.		
AAC39512.1	AF043284	Gossypium hirsutum
expansin. GhEX1. contains N-terminal signal peptide.		
AAB81662.1	U85246	Oryza sativa
expansin. Os-EXP4.		
AAG13983.1	AF297522	Prunus avium
expansin 2. Exp2. PruavExp2.		
AAF32409.1	AF230276	Triphysaria versicolor
alpha-expansin 3.		
AAG32921.1	AF184233	Lycopersicon esculentum
expansin. Exp10.		

BAB32732.1	AB049406	Eustoma grandiflorum expansin. Eg Expansin.
AAF32411.1	AF230278	Triphysaria versicolor alpha-expansin 1.
AAF35902.1	AF230333	Zinnia elegans expansin 3.
AAB38074.1	U30477	Oryza sativa induces extension (creep) in plant cell walls. expansin Os-EXP2. Os-EXP2. former gene name RiExB.
AAC96080.1	AF049353	Nicotiana tabacum involved in acid-growth response. alpha-expansin precursor. Nt-EXP4. cell wall protein.
AAF17570.1	AF202119	Marsilea quadrifolia alpha-expansin. EXP1. Mq-EXP1.
CAC06433.1	AJ276007	Festuca pratensis expansin. exp2.
AAD13633.1	AF059489	Lycopersicon esculentum expansin precursor. Exp5.
CAC19183.1	AJ291816	Cicer arietinum expansin.
AAF62181.1	AF247163	Oryza sativa alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.
AAF62180.1	AF247162	Oryza sativa alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.
CAB46492.1	AJ243340	Lycopersicon esculentum expansin9. exp9.
BAA88200.1	AP000837	Oryza sativa EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
AAF32410.1	AF230277	Triphysaria versicolor alpha-expansin 2.
AAB37749.1	U30460	Cucumis sativus expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
CAA04385.1	AJ000885	Brassica napus Cell wall extension in plants. Expansin.
AAF17571.1	AF202120	Regnellidium diphyllum alpha-expansin. EXP1. Rd-EXP1.
AAD13632.1	AF059488	Lycopersicon esculentum expansin precursor. Exp4.
CAA06271.2	AJ004997	Lycopersicon esculentum expansin18. exp18.

AAC63088.1	U82123	<i>Lycopersicon esculentum</i>	expansin. LeEXP1. fruit ripening regulated expansin.
AAC96077.1	AF049350	<i>Nicotiana tabacum</i>	involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
AAF62182.1	AF247164	<i>Oryza sativa</i>	alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.
CAC18802.1	AJ289154	<i>Glycine max</i>	expansion of cell walls. expansin. dd2/63.
AAC96078.1	AF049351	<i>Nicotiana tabacum</i>	involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
AAG01875.1	AF291659	<i>Striga asiatica</i>	alpha-expansin 3. Exp3.
CAA69105.1	Y07782	<i>Oryza sativa</i>	expansin. RiExA.
AAC96079.1	AF049352	<i>Nicotiana tabacum</i>	involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.
SEQ ID NO: 833			
AAA34030.1	J03492	<i>Spinacia oleracea</i>	glycolate oxidase (EC 1.1.3.15).
AAB40396.1	U80071	<i>Mesembryanthemum crystallinum</i>	glycolate oxidase. GOX.
BAA03131.1	D14044	<i>Cucurbita</i> sp.	glycolate oxidase.
AAB82143.1	AF022740	<i>Oryza sativa</i>	glycolate oxidase. GOX.
CAA63482.1	X92888	<i>Lycopersicon esculentum</i>	conversion of glycolate to glyoxylate + H <sub>2</sub> O <sub>2</sub> . glycolate oxidase.
AAC32392.1	AF082874	<i>Medicago sativa</i>	glycolate oxidase.
AAC33509.1	U62485	<i>Nicotiana tabacum</i>	photorespiration. glycolate oxidase. GLO.
AAF03097.1	AF162196	<i>Lactuca sativa</i>	glycolate oxidase.
SEQ ID NO: 838			
CAA06770.1	AJ005928	<i>Brassica napus</i>	squalene epoxidase homologue. Sqp1;2.
CAA06773.1	AJ005931	<i>Brassica napus</i>	squalene epoxidase homologue. Sqp1;1.
BAA24448.1	AB003516	<i>Panax ginseng</i>	squalene epoxidase.
CAA06223.1	AJ004923	<i>Lycopersicon esculentum</i>	Squalene epoxidase. ERG.

## SEQ ID NO: 840

BAB12686.1 AP002746 *Oryza sativa*  
putative pyrophosphate-dependent phosphofructo-1-kinase. P0671B11.1. contains ESTs  
AU068014(C11507),C28532(C61484),AU090544(C61415).

BAA99438.1 AP002743 *Oryza sativa*  
putative pyrophosphate-dependent phosphofructo-1-kinase. P0710E05.25. contains ESTs  
AU068014(C11507),C28532(C61484),AU090544(C61415).

AAB88875.1 U93272 *Prunus armeniaca*  
pyrophosphate-dependent phosphofructo-1-kinase.

CAA83683.1 Z32850 *Ricinus communis*  
pyrophosphate-dependent phosphofructokinase beta subunit.

AAC67587.1 AF095521 *Citrus x paradisi*  
pyrophosphate-dependent phosphofructokinase alpha subunit. PPI-PFKa.

AAA63452.1 M55191 *Solanum tuberosum*  
pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta-subunit.

AAC67586.1 AF095520 *Citrus x paradisi*  
pyrophosphate-dependent phosphofructokinase beta subunit. PPI-PFKb. PFP.

AAA63451.1 M55190 *Solanum tuberosum*  
pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha-subunit.

CAA83682.1 Z32849 *Ricinus communis*  
pyrophosphate-dependent phosphofructokinase alpha subunit.

## SEQ ID NO: 841

AAG60182.1 AC084763 *Oryza sativa*  
putative ethylene-responsive element binding protein. OSJNBa0027P10.12.

AAK31279.1 AC079890 *Oryza sativa*  
putative ethylene-responsive element binding protein. OSJNBb0089A17.16.

AAG43545.1 AF211527 *Nicotiana tabacum*  
Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.

AAF63205.1 AF245119 *Mesembryanthemum crystallinum*  
AP2-related transcription factor. CDBP. stress induced transcription factor.

BAA07321.1 D38123 *Nicotiana tabacum*  
ERF1. ethylene-responsive transcription factor.

BAA97122.1 AB016264 *Nicotiana sylvestris*  
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-  
related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

CAB93940.1 AJ238740 *Catharanthus roseus*  
putative transcription factor. AP2-domain DNA-binding protein. orca2.

BAA87068.1 AB035270 *Matricaria chamomilla*  
ethylene-responsive element binding protein1 homolog. McEREBP1.

BAA97124.1 AB016266 *Nicotiana sylvestris*  
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-  
related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

CAB96900.1	AJ251250	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
CAB96899.1	AJ251249	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
AAC62619.1	AF057373	Nicotiana tabacum	transcription factor. ethylene response element binding protein 1. EREBP1.
BAA97123.1	AB016265	Nicotiana glauca	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
AAC24587.1	AF071893	Prunus armeniaca	AP2 domain containing protein. AP2DCP.
CAC12822.1	AJ299252	Nicotiana tabacum	AP2 domain-containing transcription factor. ap2.
AAF76898.1	AF274033	Atriplex hortensis	apetala2 domain-containing protein.
BAA94514.2	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4, BAC clone F9D16; putative Ap2 domain protein (AL035394).
AAC14323.1	AF058827	Nicotiana tabacum	TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.
AAD00708.1	U91857	Stylosanthes hamata	ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
BAA76734.1	AB024575	Nicotiana tabacum	ethylene responsive element binding factor.
BAB03248.1	AB037183	Oryza sativa	ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
BAB16083.1	AB036883	Oryza sativa	transcriptional repressor. osERF3. ERF protein family ERF3 associated repression domain.
AAF23899.1	AF193803	Oryza sativa	transcription factor EREBP1. EREBP/AP2-like transcription factor.
AAF05606.1	AF190770	Oryza sativa	EREBP-like protein. tsh1. TSH1; induced by ethylene.
CAB93939.1	AJ238739	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca1.
BAA78738.1	AB023482	Oryza sativa	EST AU055776(S20048) corresponds to a region of the predicted gene.; Similar to Arabidopsis thaliana AP2 domain containing protein RAP2.10 mRNA, partial cds.(AF003103).
AAG43548.1	AF211530	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.

AAG43549.1	AF211531	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
BAA99376.1	AP002526	Oryza sativa	ESTs AU093391(E60370),AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana BAC F21J9; AP2 domain protein. (AC000103).
AAK31271.1	AC079890	Oryza sativa	putative transcriptional factor. OSJNBb0089A17.22.
AAK01089.1	AF298231	Hordeum vulgare	CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.
AAG59618.1	AF239616	Hordeum vulgare	CRT/DRE-binding factor. CBF.
AAC49567.1	U41466	Zea mays	Glossy15. Glossy15. AP2 DNA-binding domain protein; similar to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.
SEQ ID NO: 842			
AAC32034.1	AF023472	Hordeum vulgare	peptide transporter. ptr1. PTR1; integral membrane protein.
BAB40113.1	AP003311	Oryza sativa	putative peptide transport protein. P0024G09.4. contains ESTs D40448(S2437),C71800(E0368),AU102190(E2393), AU055921(S20154),AU102191(E2393),AU055922(S20154), C98524(E0368),AU097146(S2437).
BAB16458.1	AP002483	Oryza sativa	putative peptide transport protein. P0019D06.16. contains ESTs D40448(S2437),C71800(E0368),AU102190(E2393), AU055921(S20154),AU102191(E2393),AU055922(S20154), C98524(E0368),AU097146(S2437).
AAD01600.1	AF016713	Lycopersicon esculentum	LeOPT1. LeOPT1. oligopeptide transporter.
AAF07875.1	AF140606	Oryza sativa	nitrate transporter. NRT1.
AAF20002.1	AF213936	Prunus dulcis	amino acid/peptide transporter. PTR2. similar to transporters of nitrogenous compounds.
AAG46153.1	AC018727	Oryza sativa	putative peptide transporter. OSJNBa0056G17.8.
CAC00544.1	AJ277084	Nicotiana plumbaginifolia	ion transport. putative low-affinity nitrate transporter. nrt1.1.
CAC00545.1	AJ277085	Nicotiana plumbaginifolia	ion transport. putative low-affinity nitrate transporter. nrt1.2.
AAA80582.1	U17987	Brassica napus	putative nitrate transporter. RCH2 protein.

CAC07206.1	AJ278966	Brassica napus	Low-affinity nitrate transporter. nitrate transporter. nrt1.
AAG21898.1	AC026815	Oryza sativa	putative peptide transport protein. OSJNBa0079L16.13.
BAB19758.1	AB052786	Glycine max	putative nitrate transporter NRT1-3. NRT1-3.
AAK15441.1	AC037426	Oryza sativa	putative nitrate transporter. OSJNBb0014I11.9.
AAG21906.1	AC026815	Oryza sativa	putative peptide transport protein. OSJNBa0079L16.9.
BAB19760.1	AB052788	Glycine max	nitrate transporter NRT1-5. NRT1-5.
AAG46154.1	AC018727	Oryza sativa	putative peptide transporter. OSJNBa0056G17.27.
BAB19757.1	AB052785	Glycine max	nitrate transporter NRT1-2. NRT1-2.
BAB19756.1	AB052784	Glycine max	nitrate transporter NRT1-1. NRT1-1.
BAB16322.1	AP002818	Oryza sativa	putative peptide transporter-like protein. P0436E04.4.
AAB69642.1	AF000392	Lotus japonicus	peptide transporter. LjNOD65.
CAA93316.1	Z69370	Cucumis sativus	nitrite transporter. NiTR1.
AAD16016.1	AF080545	Nepenthes alata	peptide transporter. PTR1.
BAB19759.1	AB052787	Glycine max	putative nitrate transporter NRT1-4. NRT1-4.
AAD42860.1	AF154930	Prunus dulcis	transporter-like protein. TLP1.
SEQ ID NO: 847			
CAA61980.1	X89890	Bidens pilosa	Calmodulin.
AAF73157.1	AF150059	Brassica napus	calmodulin. CaM1. involved in seed germination.
BAA87825.1	AP000815	Oryza sativa	ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene. Similar to O.sativa gene encoding calmodulin. (Z12828).
CAA67054.1	X98404	Capsicum annuum	calmodulin-2.
AAA87347.1	M88307	Brassica juncea	calmodulin.



AAA33397.1	L18912	<i>Lilium longiflorum</i> calcium binding protein, signal transduction. calmodulin. putative.
AAG27432.1	AF295637	<i>Elaeis guineensis</i> calmodulin.
CAA42423.1	X59751	<i>Daucus carota</i> calmodulin. Ccam-1.
AAG11418.1	AF292108	<i>Prunus avium</i> calmodulin.
AAA92681.1	U13882	<i>Pisum sativum</i> calcium-binding protein. calmodulin.
AAB46588.1	U83402	<i>Capsicum annuum</i> calmodulin.
AAA33706.1	M80836	<i>Petunia x hybrida</i> calmodulin. CAM81.
AAF65511.1	AF108889	<i>Capsicum annuum</i> calmodulin.
CAA43143.1	X60738	<i>Malus x domestica</i> Calmodulin. CaM.
AAA19571.1	U10150	<i>Brassica napus</i> calcium binding. calmodulin. bcm1.
CAA78301.1	Z12839	<i>Lilium longiflorum</i> calcium binding protein, signal transduction. calmodulin.
BAA88540.1	AP000969	<i>Oryza sativa</i> ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene. Similar to calmodulin. (AF042840).
AAB36130.1	S81594	<i>Vigna radiata</i> auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from Fig. 1; arCaM.
AAC36059.1	AF042840	<i>Oryza sativa</i> calmodulin. CaM1.
AAA33901.1	L18913	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin. putative.
AAA33900.1	L18914	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin.
AAA34237.1	L20691	<i>Vigna radiata</i> calmodulin.
CAA78288.1	Z12828	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin.
AAA32938.1	M27303	<i>Hordeum vulgare</i> calmodulin.
CAA78287.1	Z12827	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin.

AAC49587.1	U49105	Triticum aestivum calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	Triticum aestivum calmodulin TaCaM3-3. calcium-binding protein.
AAC49583.1	U48692	Triticum aestivum calmodulin TaCaM2-3. calcium-binding protein.
AAC49585.1	U49103	Triticum aestivum calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum calmodulin TaCaM3-1. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum calmodulin TaCaM2-2. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	Triticum aestivum calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	Triticum aestivum calmodulin TaCaM1-1. calcium-binding.
AAA03580.1	L01431	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-2. putative.
AAC36058.1	AF042839	Oryza sativa calmodulin. CaM2.
AAA85156.1	U20296	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34014.1	L01432	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAD10244.1	AF030032	Phaseolus vulgaris calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
CAA36644.1	X52398	Medicago sativa calmodulin (AA 1-149).
AAA85155.1	U20294	Solanum tuberosum calcium-binding protein. calmodulin.
AAB68399.1	U79736	Helianthus annuus calmodulin. HaCaM.
AAA62351.1	U20295	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34238.1	L20507	Vigna radiata calmodulin.
AAA85157.1	U20297	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34013.1	L01430	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-1. putative.

AAA33705.1	M80831	Petunia x hybrida	calmodulin-related protein. CAM53.
CAA74307.1	Y13974	Zea mays	calmodulin.
CAA54583.1	X77397	Zea mays	calmodulin. CaM2.
SEQ ID NO: 848			
CAA06486.1	AJ005340	Linum usitatissimum	IAA amidohydrolase. homolog.
SEQ ID NO: 850			
BAB17350.1	AP002747	Oryza sativa	putative nodulin. P0698G03.34. contains ESTs D39891(S1543),D41717(S4395),AU033037(S1543).
BAA85440.1	AP000616	Oryza sativa	ESTs AU055729(S20023),AU055730(S20023) correspond to a region of the predicted gene.; similar to Medicago nodulin N21-like protein (AC004218).
CAB53493.1	AJ245900	Oryza sativa	CAA303720.1 protein. q3037.20. Similar to Medicago nodulin N21 (MtN21).
SEQ ID NO: 852			
AAD16018.1	AF081514	Taxus canadensis	prenyltransferase. geranylgeranyl diphosphate synthase. geranylgeranyl pyrophosphate synthase.
SEQ ID NO: 853			
BAB32588.1	AB055807	Momordica charantia	inhibitor against trypsin. bgit.
AAA34180.1	J05094	Lycopersicon peruvianum	proteinase inhibitor I precursor.
AAA34198.1	M59427	Lycopersicon peruvianum	proteinase inhibitor I. proteinase inhibitor I.
CAB61327.1	AJ132473	Amaranthus hypochondriacus	Proteinase inhibition. trypsin inhibitor.
AAA60745.1	J04099	Lycopersicon esculentum	proteinase inhibitor I. ER1.
CAA78269.1	Z12623	Nicotiana tabacum	Putative precursor of serine proteinase inhibitor type I. Pre-pro-proteinase inhibitor I.
CAA47461.1	X67076	Nicotiana tabacum	inhibitor of microbial serine proteinases (major isoform). TIMPa.
CAA78265.1	Z12619	Nicotiana tabacum	precursor for serine proteinase inhibitor I. Pre-pro-proteinase inhibitor I.
CAA47460.1	X67075	Nicotiana tabacum	inhibitor of microbial serine proteinases (minor isoform). TIMPb.
AAA34067.1	M74102	Nicotiana sylvestris	pre-pro-proteinase inhibitor I.

AAC49603.1	U30861	Solanum tuberosum	serine proteinase inhibitor. wound-inducible proteinase inhibitor I.
BAA02823.1	D13662	Nicotiana glauca X Nicotiana langsdorffii	genetic tumor-related proteinase inhibitor I precursor. GTI.
AAA34199.1	K03290	Lycopersicon esculentum	wound-induced proteinase inhibitor I prepropeptide.
AAA34200.1	M13938	Lycopersicon esculentum	proteinase inhibitor I. PIIF.
AAA69780.1	L06137	Solanum tuberosum	proteinase inhibitor I. pin1. putative.
AAA72133.1	L06985	Solanum tuberosum	proteinase inhibitor I. pin1. The 'a' of the first atg is missing.
CAA78259.1	Z12611	Solanum tuberosum	proteinase inhibitor I.
AAA69781.1	L06606	Solanum tuberosum	proteinase inhibitor I. precursor.
CAA48136.1	X67950	Solanum tuberosum	protease inhibitor I. pin1.
CAA47907.1	X67675	Solanum tuberosum	proteinase inhibitor I. pin1.
CAB71340.1	AJ250663	Hordeum vulgare	putative proteinase inhibitor. bci-7. similarity to subtilisin/chymotrypsin inhibitor.
CAA57677.1	X82187	Zea mays	serine proteinase inhibitor. substilin /chymotrypsin-like inhibitor. pis7.
CAA55588.1	X78988	Zea mays	proteinase inhibitor. MPI.
CAA49593.1	X69972	Zea mays	proteinase inhibitor. MPI.
AAA33816.1	M17108	Solanum tuberosum	proteinase inhibitor I. precursor.
CAA57307.1	X81647	Cucurbita maxima	Pumpkin fruit trypsin inhibitor. pfiAF4.
CAA57203.1	X81447	Cucurbita maxima	Pumpkin Fruit Chymotrypsin Inhibitor. pfiBM7.
SEQ ID NO: 859			
AAC34855.1	AF082030	Hemerocallis hybrid cultivar	senescence-associated protein 5. SA5. mRNA accumulates in senescing petals and accumulation is induced by exogenous ABA.
AAG13616.1	AC078840	Oryza sativa	putative senescence-associated protein. OSJNBb0073N24.21.
SEQ ID NO: 864			
AAF62403.1	AF212183	Nicotiana tabacum	harpin inducing protein. hin1. similar to hin1 protein.

CAA68848.1	Y07563	Nicotiana tabacum	activated during hypersensitive response. hin1.
AAB97367.1	AF039532	Oryza sativa	harpin induced gene 1 homolog. Hin1.
SEQ ID NO: 871			
AAC61839.1	AF025430	Papaver somniferum	berberine bridge enzyme. bbe1. (S)-reticuline:oxygen oxidoreductase (methylene bridge forming).
AAB20352.1	S65550	Eschscholzia californica	(S)-reticuline:oxygen oxidoreductase (methylene-bridge-forming). /gene="(S)-reticuline:oxygen oxidoreductase. This sequence comes from Fig 2; berberine bridge enzyme.
AAC39358.1	AF005655	Eschscholzia californica	oxidizes the N-methyl group of (S)-reticuline to the berberine bridge carbon C-8 of (S)-scoulerine in berberine and benzophenanthridine alkaloid biosynthesis. berberine bridge enzyme. bbe1. covalently-bound FAD-dependent oxidase; elicitor-inducible.
AAD17487.1	AF049347	Berberis stolonifera	Catalyzes the oxidative cyclization of the N-methyl group of (S)-reticuline into the berberine bridge carbon (C-8) of (S)-scoulerine. berberine bridge enzyme. bbe1. Covalently flavinylated oxidase of isoquinoline alkaloid biosynthesis in plants.
SEQ ID NO: 872			
AAF98369.1	AF158253	Nicotiana tabacum	patatin-like protein 3. PAT3. NtPat3.
CAA73328.1	Y12793	Cucumis sativus	mobilization of fat during seed germination. patatin-like protein.
CAA11042.1	AJ223039	Hevea brasiliensis	latex allergen. sequence similarity to patatins.
AAF25553.1	AF113546	Hevea brasiliensis	latex protein allergen Hev b 7. putative PLA2; similar to Solanum tubulin patatin encoded by GenBank Accession Number X03932.
CAA11041.1	AJ223038	Hevea brasiliensis	latex allergen. with sequence similarity to patatins.
AAC27724.1	U80598	Hevea brasiliensis	latex patatin homolog. putative PLA2; latex protein allergen; similar to Solanum tubulin patatin encoded by GenBank Accession Number X03932.
AAK27797.1	AF318315	Vigna unguiculata	patatin-like protein.
AAK18751.1	AF193067	Vigna unguiculata	patatin-like protein.
AAB08428.1	U68484	Nicotiana tabacum	patatin homolog.
AAD22170.1	AF061282	Sorghum bicolor	patatin-like protein.

AAF98368.1	AF158027	Nicotiana tabacum	patatin-like protein 1. PAT1. NtPat1.
AAD22169.1	AF061282	Sorghum bicolor	patatin-like protein.
CAA81735.1	Z27221	Solanum tuberosum	patatin.
CAA31575.1	X13178	Solanum tuberosum	patatin B2 (AA 1 - 386).
AAA33819.1	M18880	Solanum tuberosum	patatin.
CAA31576.1	X13179	Solanum tuberosum	patatin B1 (377 AA) (1 is 3rd base in codon).
CAA27588.1	X03956	Solanum tuberosum	patatin.
AAA33828.1	M21879	Solanum tuberosum	patatin.
CAA27571.1	X03932	Solanum tuberosum	patatin.
CAA25592.1	X01125	Solanum tuberosum	patatin.
AAA66198.1	U09331	Solanum brevidens	patatin precursor.
AAB08427.1	U68483	Nicotiana tabacum	patatin homolog.
AAF98370.1	AF158254	Nicotiana tabacum	patatin-like protein 2. PAT2.
AAD22149.1	AF061282	Sorghum bicolor	patatin-like protein. similar to the EST sequences E0496(panicle at flowering stage), R2382 (root), R2382 (root), S4036 (shoot), S3728 (shoot), S13457 (green shoot).
SEQ ID NO: 875			
BAA93022.1	AP001552	Oryza sativa	ESTs C74776(E51022),C26123(C116681) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana cultivar Landsberg extra-large G-protein (AF060942).
SEQ ID NO: 876			
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.

BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
BAA82556.1	AB030083	Populus nigra	lectin-like protein kinase. PnLPK.
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
AAB09771.1	U67422	Zea mays	CRINKLY4 precursor. cr4. receptor kinase homolog.
AAF34428.1	AF172282	Oryza sativa	receptor-like protein kinase. DUPR11.18.
BAB07906.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.14.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
BAA94516.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).

AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
BAA06538.1	D31737	Nicotiana tabacum	protein-serine/threonine kinase.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
BAB07904.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.12.
BAA94518.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.



BAB03429.1 AP002817 *Oryza sativa*  
EST C22619(S11214) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).

SEQ ID NO: 883

BAA90510.2 AP001111 *Oryza sativa*  
rice EST AU030811, similar to rice Ca<sup>2+</sup>-ATPase (U82966).

AAF73985.1 AF096871 *Zea mays*  
calcium pump. calcium ATPase. cap1.

CAA63790.1 X93592 *Dunaliella bioculata*  
P-type ATPase. ca1. calcium pumping; CA1.

AAD11618.1 AF050496 *Lycopersicon esculentum*  
Ca<sup>2+</sup>-ATPase. LCA1B; alternative transcript.

AAA34138.1 M96324 *Lycopersicon esculentum*  
The calcium ATPase is a calcium ion pump. Ca<sup>2+</sup>-ATPase. LCA1.

AAB58910.1 U82966 *Oryza sativa*  
Ca<sup>2+</sup>-ATPase.

AAD11617.1 AF050495 *Lycopersicon esculentum*  
Ca<sup>2+</sup>-ATPase. LCA1A; alternative transcript.

AAG28435.1 AF195028 *Glycine max*  
plasma membrane Ca<sup>2+</sup>-ATPase. SCA1.

AAG28436.1 AF195029 *Glycine max*  
plasma membrane Ca<sup>2+</sup>-ATPase. SCA2.

CAA68234.1 X99972 *Brassica oleracea*  
calmodulin-stimulated calcium-ATPase.

AAD31896.1 AF145478 *Mesembryanthemum crystallinum*  
calcium ATPase.

AAB60276.1 U09989 *Zea mays*  
H(+)-transporting ATPase. Mha1.

CAB69824.1 AJ271439 *Prunus persica*  
plasma membrane H<sup>+</sup> ATPase. PPA1.

AAD46187.1 AF156683 *Nicotiana plumbaginifolia*  
plasma membrane proton ATPase. pma8.

BAA01058.1 D10207 *Oryza sativa*  
H-ATPase. OSA1.

AAB49042.1 U54690 *Dunaliella acidophila*  
plasma membrane proton ATPase. dha1. DaDHA1; proton pump.

AAA34173.1 M60166 *Lycopersicon esculentum*  
H<sup>+</sup>-ATPase. LHA1.

CAA52107.1 X73901 *Dunaliella bioculata*  
plasma membrane ATPase. pma1.

AAB35314.2	S79323	<i>Vicia faba</i>	plasma membrane H(+)-ATPase precursor. plasma membrane H(+)-ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.
BAA06629.1	D31843	<i>Oryza sativa</i>	plasma membrane H <sup>+</sup> -ATPase. OSA2.
AAA34094.1	M80489	<i>Nicotiana plumbaginifolia</i>	plasma membrane H <sup>+</sup> ATPase. pma1.
BAA08134.1	D45189	<i>Zostera marina</i>	plasma membrane H <sup>+</sup> -ATPase. zha1.
CAB85494.1	AJ132891	<i>Medicago truncatula</i>	proton pump. H <sup>+</sup> -ATPase. ha1.
CAB85495.1	AJ132892	<i>Medicago truncatula</i>	proton pump. H <sup>+</sup> -ATPase. ha1.
AAB84202.2	AF029256	<i>Kosteletzkya virginica</i>	plasma membrane proton ATPase. ATP1.
CAA47275.1	X66737	<i>Nicotiana plumbaginifolia</i>	plasma membrane H <sup>+</sup> -ATPase. pma4.
CAA54045.1	X76535	<i>Solanum tuberosum</i>	H(+)-transporting ATPase. PHA2.
AAD46186.1	AF156679	<i>Nicotiana plumbaginifolia</i>	plasma membrane proton ATPase. pma6.
AAB17186.1	U72148	<i>Lycopersicon esculentum</i>	plasma membrane H <sup>+</sup> -ATPase. LHA4. plasma membrane proton pumping ATPase.
CAB69823.1	AJ271438	<i>Prunus persica</i>	plasma membrane H <sup>+</sup> ATPase. PPA2.
AAB41898.1	U84891	<i>Mesembryanthemum crystallinum</i>	plasma membrane proton pump. H <sup>+</sup> -transporting ATPase. PMA.
CAC29436.1	AJ310524	<i>Vicia faba</i>	P-type H <sup>+</sup> -ATPase. ha5. predominantly expressed in guard cells and flowers.
BAA37150.1	AB022442	<i>Vicia faba</i>	p-type H <sup>+</sup> -ATPase. VHA2.
CAA59800.1	X85805	<i>Zea mays</i>	H(+)-transporting ATPase. MHA-2.
CAA59799.1	X85804	<i>Phaseolus vulgaris</i>	H(+)-transporting ATPase. BHA-1.
CAC29435.1	AJ310523	<i>Vicia faba</i>	P-type H <sup>+</sup> -ATPase. vha4. predominantly expressed in flowers.
AAD46188.1	AF156691	<i>Nicotiana plumbaginifolia</i>	plasma membrane proton ATPase. pma9.
AAA34099.1	M80491	<i>Nicotiana plumbaginifolia</i>	plasma membrane H <sup>+</sup> ATPase. pma3.

AAA34052.1	M27888	Nicotiana plumbaginifolia	H <sup>+</sup> -translocating ATPase.
CAA54046.1	X76536	Solanum tuberosum	H(+)-transporting ATPase. PHA1.
AAA34098.1	M80490	Nicotiana plumbaginifolia	plasma membrane H <sup>+</sup> ATPase. pma3.
AAD55399.1	AF179442	Lycopersicon esculentum	plasma membrane H <sup>+</sup> -ATPase isoform LHA2. LHA2.
AAF98344.1	AF275745	Lycopersicon esculentum	plasma membrane H <sup>+</sup> -ATPase. LHA2. P-type ion pump.
AAG01028.1	AF289025	Cucumis sativus	plasma membrane H <sup>+</sup> -ATPase.
AAK31799.1	AY029190	Lilium longiflorum	plasma membrane H <sup>+</sup> ATPase. LILHA1.
AAA81348.1	U38965	Vicia faba	p-type H <sup>+</sup> -ATPase. VHA2.
AAK32119.1	AF308817	Hordeum vulgare	plasmalemma H <sup>+</sup> -ATPase 2.
AAK32118.1	AF308816	Hordeum vulgare	plasmalemma H <sup>+</sup> -ATPase 1.
AAA20600.1	U08984	Zea mays	plasma-membrane H <sup>+</sup> ATPase. Zmpma1.
SEQ ID NO: 884			
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.

CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrkl.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
AAK02023.1	AC074283	Oryza sativa	Putative protein kinase-like. OSJNBa0087H07.5.
CAA79324.1	Z18884	Brassica oleracea	S-receptor kinase related protein.
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
CAB51836.1	AJ243961	Oryza sativa	Putitive Ser/Thr protein kinase. 11332.7.
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
BAB17139.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.31.
SEQ ID NO: 885			
CAA80358.1	Z22645	Solanum tuberosum	cleavage of sucrose to glucose and fructose. beta-fructofuranosidase.
CAA79676.1	Z21486	Solanum tuberosum	cleavage of sucrose to glucose and fructose. beta-fructofuranosidase.
CAA57428.1	X81834	Nicotiana tabacum	beta-fructofuranosidase. Ntbfruc1. beta-fructosidase.
CAA49162.1	X69321	Daucus carota	beta-fructofuranosidase. Inva1*DC1.
CAA57389.1	X81792	Chenopodium rubrum	beta-fructofuranosidase. CIN1.
AAC17166.1	AF063246	Pisum sativum	hydrolyzes sucrose to glucose and fructose. cell wall invertase. bfruct1. isoform Pcl-2; the Pcl-1 isoform is in the file with GenBank Accession Number X85327; beta-fructofuranosidase.
CAA59677.1	X85327	Pisum sativum	hydrplyze sucrose into fructose and glucose. invertase. bfruct1. beta-fructofuranosidase.
AAD02263.1	AF043346	Zea mays	sucrose hydrolysis. cell wall invertase. incw3. Incw3; beta-fructofuranosidase.
CAA84526.1	Z35162	Vicia faba	hydrolyze sucrose. beta-fructofuranosidase; cell wall invertase I; fructosidase. VFCWINV1.

AAC96065.1	AF030420	Triticum aestivum	hydrolyzes sucrose. cell wall invertase. IVR1. hydrolase; beta-fructofuranosidase; fructosidase.
CAA53099.1	X75353	Daucus carota	beta-fructofuranosidase.
AAB68679.1	U92438	Phaseolus vulgaris	soluble acid invertase. PVSAI; potential vacuolar targeted enzyme; beta-fructofuranosidase.
CAA89992.1	Z49831	Vicia faba	hydrolyze sucrose. vacuolar invertase; beta-fructofuranosidase. VFVCINV.
CAA53097.1	X75351	Daucus carota	beta-fructofuranosidase.
CAA77267.1	Y18707	Daucus carota	beta-fructofuranosidase, isoform I. Inv*Dc4. soluble acid invertase.
CAA53098.1	X75352	Daucus carota	beta-fructofuranosidase.
CAA77266.1	Y18706	Daucus carota	beta-fructofuranosidase, isoform II. Inv*Dc5. soluble acid invertase.
AAC96066.1	AF030421	Triticum aestivum	hydrolyzes sucrose. cell wall invertase. IVR3. hydrolase; beta-fructofuranosidase; fructosidase.
AAG36943.1	AF274299	Brassica oleracea	cleaves sucrose into glucose and fructose at acid pH optima. acid invertase AI7-3. sucrose hydrolysing enzyme; beta-fructofuranosidase.
SEQ ID NO: 887			
AAD10836.1	U52079	Solanum tuberosum	P-glycoprotein. pmdr1. binds ATP; ATPase; transporter; transmembrane protein.
BAA96612.1	AP002482	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2, BAC F14M4 ; putative ABC transporter (AC004411).
AAG49002.1	AY013246	Hordeum vulgare	putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative sequencing.
AAG45492.1	AY013245	Oryza sativa	36I5.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and comparative sequence.
BAA83352.1	AP000391	Oryza sativa	ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.; Similar to ABC transporter-7 (U43892).
AAG49003.1	AY013246	Hordeum vulgare	putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and comparative sequence.
BAB17113.1	AP002866	Oryza sativa	putative white protein; ATP-binding cassette transporter. P0410E01.34.

BAA90508.1	AP001111	Oryza sativa	similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAA90507.1	AP001111	Oryza sativa	similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAB16495.1	AP002861	Oryza sativa	putative ABC transporter ATP-binding protein. P0665D10.21.
BAB21276.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
BAB21275.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.6.
BAB21273.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.4.
BAB40032.1	AP003046	Oryza sativa	putative ABC transporter. P0445D12.3.
SEQ ID NO: 888			
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.

CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrk1.
AAK02023.1	AC074283	Oryza sativa	Putative protein kinase-like. OSJNBa0087H07.5.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
BAB17331.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.12.
BAB17139.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.31.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.



BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
CAB51836.1	AJ243961	Oryza sativa	Putative Ser/Thr protein kinase. I1332.7.
AAF78016.1	AF238472	Oryza sativa	receptor-like kinase. RLG15. protein kinase.
BAB39451.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.24.
SEQ ID NO: 890			
AAB47181.1	S82324	Zea mays	/gene="calcium/calmodulin-dependent protein kinase. This sequence comes from Fig. 1.
BAA22410.1	D38452	Zea mays	calcium-dependent protein kinase-related kinase.
BAA12692.1	D84508	Zea mays	CDPK-related protein kinase. Does not require calcium for its activity.
AAG01179.1	AF289237	Zea mays	calcium/calmodulin dependent protein kinase MCK2. MCK2.
CAA58750.1	X83869	Daucus carota	CDPK-related protein kinase. CRK (or PK421).
BAA12691.1	D84507	Zea mays	CDPK-related protein kinase. Does not require calcium for its activity (by similarity).
AAC24961.1	AF009337	Tradescantia virginiana	CDPK-related protein kinase. CRK1.
AAF23901.2	AF194414	Oryza sativa	calcium-dependent protein kinase. CDPK5. OsCDPK5.
AAF23900.1	AF194413	Oryza sativa	calcium-dependent protein kinase. CDPK1. OsCDPK1.
AAC78558.1	AF030879	Solanum tuberosum	protein kinase CPK1.
AAD17800.1	AF090835	Mesembryanthemum crystallinum	Ca <sup>2+</sup> -dependent protein kinase. CPK1. serine/threonine protein kinase.
AAB49984.1	U90262	Cucurbita pepo	calcium-dependent calmodulin-independent protein kinase CDPK. cpCPK1. serine/threonine protein kinase that is activated by direct binding of calcium.
CAA07481.1	AJ007366	Zea mays	calcium-dependent protein kinase.
BAB21081.1	AP002819	Oryza sativa	putative calcium-dependent protein kinase. P0501G01.10.
BAA12715.1	D85039	Zea mays	calcium-dependent protein kinase.

AAC25423.1	AF072908	Nicotiana tabacum	calcium-dependent protein kinase. CDPK1.
CAA39936.1	X56599	Daucus carota	calcium- dependent protein kinase. DcPK431.
CAA57157.1	X81394	Oryza sativa	calcium-dependent protein kinase. OSCPK2.
AAF21062.1	AF216527	Dunaliella tertiolecta	calcium-dependent protein kinase. CPK1; CDPK.
BAA81751.1	AB017517	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
BAA81749.1	AB017515	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
AAB88537.1	AF035944	Fragaria x ananassa	calcium-dependent protein kinase. MAX17.
BAA81750.1	AB017516	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
BAA81748.1	AB017515	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
AAA69507.1	U28376	Zea mays	calcium-dependent protein kinase. MZECDPK2.
AAA61682.1	L27484	Zea mays	calcium-dependent protein kinase. CDPK.
AAB80693.1	U69174	Glycine max	calmodulin-like domain protein kinase isoenzyme gamma. CDPK gamma.
BAA13232.1	D87042	Zea mays	Calcium-dependent protein kinase.
BAA13440.1	D87707	Ipomoea batatas	calcium dependent protein kinase. CDPK.
CAA89202.1	Z49233	Chlamydomonas eugametos	calcium-stimulated protein kinase.
AAB70706.1	U82087	Tortula ruralis	calmodulin-like domain protein kinase. TrCPK1.
AAD28192.2	AF115406	Solanum tuberosum	calcium-dependent protein kinase. CDPK; catalytic domain.
AAC49405.1	U08140	Vigna radiata	calcium dependent protein kinase. CDPK.
BAA12338.1	D84408	Zea mays	calcium dependent protein kinase. ZmCDPK1.
CAA65500.1	X96723	Medicago sativa	protein kinase. CDPK.

BAA85396.1	AP000615	Oryza sativa	ESTs C22369(C12239),C22370(C12239), AU057852(S21844),AU057853(S21844) correspond to a region of the predicted gene.; similar to calcium dependent protein kinase. (AF048691).
AAA33443.1	L15390	Zea mays	calcium-dependent protein kinase. CDPK.
AAB80692.1	U69173	Glycine max	calmodulin-like domain protein kinase isoenzyme beta. CDPK beta.
CAA57156.1	X81393	Oryza sativa	calcium-dependent protein kinase. OSCP2II.
AAC05270.1	AF048691	Oryza sativa	calcium dependent protein kinase. CDPK12.
AAK26164.1	AY027885	Cucumis sativus	calcium-dependent calmodulin-independent protein kinase 5. CDPK5. CsCDPK5.
AAG46110.1	AC073166	Oryza sativa	calcium-dependent protein kinase. OSJNBb0064P21.2.
BAA02698.1	D13436	Oryza sativa	calcium-dependent protein kinase. spk.
BAA90814.1	AP001168	Oryza sativa	ESTs AU030197(E50746),AU030196(E50746) correspond to a region of the predicted gene.; Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).
AAF19401.1	AF203479	Glycine max	phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca <sup>2+</sup> /CaM kinase family; lacks the autoinhibitory region and EF hands.
CAB46228.1	Y18055	Arachis hypogaea	calcium dependent protein kinase. CDPK.
AAF19403.1	AF203481	Lycopersicon esculentum	phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca <sup>2+</sup> /CaM kinase family; lacks the autoinhibitory region and EF hands.
AAF19402.1	AF203480	Lycopersicon esculentum	phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca <sup>2+</sup> /CaM kinase family; lacks the autoinhibitory region and EF hands.
SEQ ID NO: 892			
AAF20931.1	AF206721	Brassica juncea	ascorbate oxidase.
BAA07734.1	D43624	Nicotiana tabacum	ascorbate oxidase precursor.
AAA33119.1	J04494	Cucumis sativus	ascorbate oxidase precursor (EC 1.10.3.3).
CAA75577.1	Y15295	Medicago truncatula	L-ascorbate oxidase. MtN23.
AAF35911.2	AF233594	Cucumis melo	ascorbate oxidase AO4. multicopper oxidase.

CAA39300.1	X55779	Cucurbita sp.	ascorbate oxidase.
BAA09528.1	D55677	Cucurbita maxima	ascorbate oxidase. AAO.
AAF35910.1	AF233593	Cucumis melo	ascorbate oxidase AO1. multicopper oxidase.
CAA71275.1	Y10226	Cucumis melo	L-ascorbate oxidase. ao3.
AAF20932.1	AF206722	Brassica juncea	ascorbate oxidase.
AAF20933.1	AF206723	Brassica juncea	ascorbate oxidase.
CAA71273.1	Y10224	Cucumis melo	L-ascorbate oxidase. ao1.
CAA71274.1	Y10225	Cucumis melo	L-ascorbate oxidase. ao1.
BAA20520.1	AB004799	Oryza sativa	ascorbate oxidase.
AAF33751.1	AF202460	Capsicum annuum	ascorbic acid oxidase.
AAB17193.1	U73105	Liriodendron tulipifera	monolignol polymerization; lignin biosynthesis. laccase. LAC2-3. diphenol oxidase; blue copper oxidase.
AAB17191.1	U73103	Liriodendron tulipifera	monolignol polymerization; lignin biosynthesis. laccase. LAC2-1. diphenol oxidase; blue copper oxidase.
AAC49536.1	U43542	Nicotiana tabacum	diphenol oxidase. laccase.
AAB17194.1	U73106	Liriodendron tulipifera	monolignol polymerization; lignin biosynthesis. laccase. LAC2-4. diphenol oxidase; blue copper oxidase.
AAB17192.1	U73104	Liriodendron tulipifera	monolignol polymerization; lignin biosynthesis. laccase. LAC2-2. diphenol oxidase; blue copper oxidase.
AAC04576.1	AF047697	Oryza sativa	p-diphenol oxidase. putative high-pI laccase.
AAB09228.1	U12757	Acer pseudoplatanus	monolignol polymerization; lignin biosynthesis. laccase. diphenol oxidase.
CAA45554.1	X64257	Brassica napus	Bp10. protein homologous to ascorbate oxidase.
AAC49538.1	U45243	Nicotiana tabacum	diphenol oxidase. laccase.

AAC49537.1	U43543	Nicotiana tabacum	diphenol oxidase, laccase.
AAD02557.1	AF049931	Petunia x hybrida	PGPS/NH15. PGPS/NH15. ascorbate oxidase homolog.
SEQ ID NO: 894			
CAB43505.1	AJ239051	Cicer arietinum	cytochrome P450. cyp81E2.
BAA74465.1	AB022732	Glycyrrhiza echinata	cytochrome P450. CYP Ge-31.
BAA93634.1	AB025016	Lotus japonicus	cytochrome P450.
BAA22422.1	AB001379	Glycyrrhiza echinata	cytochrome P450. CYP81E1.
CAA04117.1	AJ000478	Helianthus tuberosus	fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'-race).
CAB41490.1	AJ238439	Cicer arietinum	cytochrome P450 monooxygenase. cyp81E3v2.
CAA04116.1	AJ000477	Helianthus tuberosus	fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
CAA10067.1	AJ012581	Cicer arietinum	cytochrome P450. cyp81E3.
AAK38079.1	AF321855	Lolium rigidum	putative cytochrome P450.
AAK38080.1	AF321856	Lolium rigidum	putative cytochrome P450.
AAK38081.1	AF321857	Lolium rigidum	putative cytochrome P450.
AAD56282.1	AF155332	Petunia x hybrida	flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAC34853.1	AF082028	Hemerocallis hybrid cultivar	putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3. mRNA accumulates in senescing petals.
AAG09208.1	AF175278	Pisum sativum	wound-inducible P450 hydroxylase. CYP82A1.
BAA12159.1	D83968	Glycine max	Cytochrome P-450 (CYP93A1).
CAA71515.1	Y10491	Glycine max	putative cytochrome P450.
CAA71876.1	Y10982	Glycine max	putative cytochrome P450.
CAA65580.1	X96784	Nicotiana tabacum	cytochrome P450. hsr515.

AAC49188.2	U29333	<i>Pisum sativum</i> cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
AAG44132.1	AF218296	<i>Pisum sativum</i> cytochrome P450. P450 isolog.
CAA71516.1	Y10492	<i>Glycine max</i> putative cytochrome P450.
CAA64635.1	X95342	<i>Nicotiana tabacum</i> cytochrome P450. hsr515. hypersensitivity-related gene.
AAC39454.1	AF014802	<i>Eschscholzia californica</i> (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome P-450-dependent, homologous to wound-inducible CYP82A1 of <i>Pisum sativum</i> GenBank Accession Number U29333.
AAB94590.1	AF022461	<i>Glycine max</i> CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
AAA32913.1	M32885	<i>Persea americana</i> cytochrome P-450LXXIA1 (cyp71A1).
CAA71877.1	Y10983	<i>Glycine max</i> putative cytochrome P450.
BAA84072.1	AB028152	<i>Torenia hybrida</i> flavone synthase II. cytochrome P450. TFNS5.
BAA13076.1	D86351	<i>Glycine max</i> cytochrome P-450 (CYP93A2).
AAG34695.1	AF313492	<i>Matthiola incana</i> putative cytochrome P450.
BAA84071.1	AB028151	<i>Antirrhinum majus</i> flavone synthase II. cytochrome P450. AFNS2.
AAC32274.1	AF081575	<i>Petunia x hybrida</i> flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.
BAA35080.1	AB015762	<i>Nicotiana tabacum</i> putative cytochrome P450. CYP82E1.
CAA50155.1	X70824	<i>Solanum melongena</i> flavonoid hydroxylase (P450). CYP75.
CAA70575.1	Y09423	<i>Nepeta racemosa</i> cytochrome P450. CYP71A5.
BAA92894.1	AB006790	<i>Petunia x hybrida</i> cytochrome P450. IMT-2.
CAA71513.1	Y10489	<i>Glycine max</i> putative cytochrome P450.
AAB94587.1	AF022458	<i>Glycine max</i> CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
SEQ ID NO: 895		

BAA78764.1	AB023482	<i>Oryza sativa</i> ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to <i>Arabidopsis thaliana</i> APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
AAF43496.1	AF131222	<i>Lophopyrum elongatum</i> protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	<i>Lophopyrum elongatum</i> protein kinase. ESI47.
AAG16628.1	AY007545	<i>Brassica napus</i> protein serine/threonine kinase BNK1.
BAA94510.1	AB041504	<i>Populus nigra</i> protein kinase 2. PnPK2.
BAA94509.1	AB041503	<i>Populus nigra</i> protein kinase 1. PnPK1.
BAA87853.1	AP000816	<i>Oryza sativa</i> EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB07999.1	AP002525	<i>Oryza sativa</i> putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB03429.1	AP002817	<i>Oryza sativa</i> EST C22619(S11214) corresponds to a region of the predicted gene. Similar to <i>Arabidopsis thaliana</i> chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB16871.1	AP002537	<i>Oryza sativa</i> putative protein kinase APK1A <i>Arabidopsis thaliana</i> . P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAB39873.1	AP002882	<i>Oryza sativa</i> putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
BAB39409.1	AP002901	<i>Oryza sativa</i> putative protein kinase. P0456F08.9. contains EST C23560(R0290).
AAK00425.1	AC069324	<i>Oryza sativa</i> Putative protein kinase. OSJNBa0071K19.11.
BAB21240.1	AP002953	<i>Oryza sativa</i> Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK21965.1	AY028699	<i>Brassica napus</i> receptor protein kinase PERK1.
AAG59657.1	AC084319	<i>Oryza sativa</i> putative protein kinase. OSJNBa0004B24.20.
AAG03090.1	AC073405	<i>Oryza sativa</i> Similar to an <i>Arabidopsis</i> somatic embryogenesis receptor-like kinase (AC007504).
CAB51834.1	00069	<i>Oryza sativa</i> 11332.5. contains eukaryotic protein kinase domain PF.

AAC61805.1	U28007	Lycopersicon esculentum	serine/threonine protein kinase. Pto kinase interactor 1. Pti1. Pti1 kinase.
AAF91336.1	AF249317	Glycine max	Pti1 kinase-like protein. Pti1a. protein kinase.
AAF91337.1	AF249318	Glycine max	Pti1 kinase-like protein. Pti1b. protein kinase.
BAB21241.1	AP002953	Oryza sativa	Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721),D48017(S13927).
AAB09771.1	U67422	Zea mays	CRINKLY4 precursor. cr4. receptor kinase homolog.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
AAF76313.1	AF220603	Lycopersicon esculentum	Pto kinase. LescPth5.
AAB47421.1	U59316	Lycopersicon esculentum	serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
BAB19337.1	AP003044	Oryza sativa	putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
AAC27894.1	AF023164	Zea mays	leucine-rich repeat transmembrane protein kinase 1. ltk1.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.



BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAA92953.1	AP001551	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).
AAK11566.1	AF318490	Lycopersicon hirsutum	Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
AAK11567.1	AF318491	Lycopersicon hirsutum	Pto-like protein kinase F. LhirPtoF.
BAA82556.1	AB030083	Populus nigra	lectin-like protein kinase. PnLPK.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
SEQ ID NO: 899			
AAF61647.1	AF190634	Nicotiana tabacum	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAA89009.1	AB027455	Petunia x hybrida	anthocyanin 5-O-glucosyltransferase. PH1.
AAA59054.1	L34847	Zea mays	conjugation of the growth hormone indole-3-acetic acid (IAA). IAA-glu synthetase. iaglu.
BAA93039.1	AB033758	Citrus unshiu	limonoid UDP-glucosyltransferase. LGTase.
BAA36423.1	AB013598	Verbena x hybrida	UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
BAA36421.1	AB013596	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
BAA36422.1	AB013597	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.
BAB07962.1	AP002524	Oryza sativa	putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
AAK16175.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.15.
AAK16181.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.16.
AAK16178.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.5.
AAG25643.1	AF303396	Phaseolus vulgaris	UDP-glucosyltransferase HRA25. putative; defense associated.

AAK16172.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.14.
BAA83484.1	AB031274	Scutellaria baicalensis	UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAB36652.1	U32643	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
AAD21086.1	AF127218	Forsythia x intermedia	adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
AAB36653.1	U32644	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS5a.
BAA12737.1	D85186	Gentiana triflora	UDP-glucose:flavonoid-3-glucosyltransferase.
AAK28303.1	AF346431	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
AAF17077.1	AF199453	Sorghum bicolor	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
AAK16180.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.21.
CAA59450.1	X85138	Lycopersicon esculentum	twil. homologous to glucosyltransferases.
BAB41017.1	AB047090	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
BAB41026.1	AB047099	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
BAB41024.1	AB047097	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT2.
BAB41022.1	AB047095	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41020.1	AB047093	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
BAA89008.1	AB027454	Petunia x hybrida	anthocyanidin 3-O-glucosyltransferase. PGT8.
BAB41018.1	AB047091	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.
CAB56231.1	Y18871	Dorothaeanthus bellidiformis	betanidin-5-O-glucosyltransferase.

AAB81683.1	AF000372	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41019.1	AB047092	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAB41025.1	AB047098	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
BAB41023.1	AB047096	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
BAB41021.1	AB047094	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
AAB81682.1	AF000371	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAA19659.1	AB002818	Perilla frutescens	flavonoid 3-O-glucosyltransferase. UDP glucose.
BAA90787.1	AB038248	Ipomoea batatas	UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.
AAD04166.1	AF101972	Phaseolus lunatus	catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
AAB86473.1	AF028237	Ipomoea purpurea	UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.
SEQ ID NO: 900			
AAA33975.1	M11395	Glycine max	small heat shock protein.
CAA41547.1	X58711	Medicago sativa	heat shock protein.
AAB03893.1	M11318	Glycine max	17.5 kd heat shock protein Gmhsp17.6L.
AAA33672.1	M33899	Pisum sativum	18.1 kDa heat shock protein (hsp18.1).
CAA25578.1	X01104	Glycine max	heat shock protein 6871 (aa 1-153).
CAB55634.2	AJ237596	Helianthus annuus	17.9 kDa heat-shock protein. hsp17.9.
BAA33062.1	AB017273	Cuscuta japonica	low-molecular-weight heat shock protein. CJHSP17.
AAA33974.1	M11317	Glycine max	17.6 kd heat shock protein Gmhsp17.6L.
AAD30454.1	AF123257	Lycopersicon esculentum	17.6 kD class I small heat shock protein. HSP17.6.
AAD30452.1	AF123255	Lycopersicon esculentum	17.7 kD class I small heat shock protein. HSP17.7.

CAA39603.1	X56138	Lycopersicon esculentum	small heat shock protein (class I).
AAD30453.1	AF123256	Lycopersicon esculentum	17.8 kD class I small heat shock protein. HSP17.8.
CAA37847.1	X53851	Daucus carota	heat shock protein.
AAA33671.1	M33900	Pisum sativum	17.9 kDa heat shock protein (hsp17.9).
AAF34133.1	AF161179	Malus x domestica	low molecular weight heat shock protein. Hsp1.
CAA41546.1	X58710	Medicago sativa	heat shock protein.
AAB63310.1	U46544	Helianthus annuus	18.6 kDa heat-shock protein. Class I low-molecular-weight heat-shock protein.
AAB63311.1	U46545	Helianthus annuus	17.7 kDa heat shock protein. Class I low-molecular-weight heat-shock protein.
CAB08441.1	Z95153	Helianthus annuus	17.6 kD class I small heat-shock protein HSP17.6. Ha hsp17.6.
CAA42222.1	X59701	Helianthus annuus	17.6 kDa heat shock protein.
AAC39360.1	U63631	Fragaria x ananassa	LMW heat shock protein.
AAA33910.1	M80939	Oryza sativa	16.9 kDa heat shock protein.
CAA37848.1	X53852	Daucus carota	heat shock protein.
AAA33909.1	M80938	Oryza sativa	16.9 kDa heat shock protein.
CAA43210.1	X60820	Oryza sativa	16.9 KD low molecular weight heat shock protein.
CAA37864.1	X53870	Chenopodium rubrum	heat-shock protein.
AAD49336.1	AF166277	Nicotiana tabacum	low molecular weight heat-shock protein. LHS-1. TLHS-1.
AAA61632.1	U08601	Papaver somniferum	low molecular weight heat-shock protein.
AAB72109.1	AF022217	Brassica rapa	low molecular weight heat-shock protein. BcHSP17.6. 17.6 kDa; cytosolic class I.
CAA63902.1	X94192	Pennisetum glaucum	heat shock protein 16.9. hsp16.9.
AAB39856.1	U81385	Oryza sativa	heat shock protein. Oshsp16.9C. class I, low molecular mass.

CAA46641.1	X65725	<i>Zea mays</i>	heat shock protein 17.2. Zmhs17.2. Class I low molecular weight heat shock protein.
CAA08908.1	AJ009880	<i>Castanea sativa</i>	molecular chaperone. cytosolic class I small heat-shock protein HSP17.5. hsp17.5.
CAB93512.1	AJ243565	<i>Brassica oleracea</i>	putative class I small heat shock protein. HSP17.7-a protein. hsp17.7-a.
CAA63903.1	X94193	<i>Pennisetum glaucum</i>	heat shock protein 17.9. hsp17.9.
CAB36910.1	AJ000691	<i>Quercus suber</i>	stress protein chaperone. heat shock protein 17.4. hsp17.
CAA63901.1	X94191	<i>Pennisetum glaucum</i>	heat shock protein 17.0. hsp17.0.
AAC78392.1	U83669	<i>Oryza sativa</i>	low molecular mass heat shock protein Oshsp17.3. OSHSP17.3. class I LMMHSP.
BAA02160.1	D12635	<i>Oryza sativa</i>	'low molecular weight heat shock protein'.
AAC78393.1	U83670	<i>Oryza sativa</i>	low molecular mass heat shock protein Oshsp18.0. OSHSP18.0. class I LMMHSP.
CAA31785.1	X13431	<i>Triticum aestivum</i>	put. heat shock protein (AA 1 -151).
CAA63570.1	X92983	<i>Pseudotsuga menziesii</i>	low molecular weight heat-shock protein.
AAC78394.1	U83671	<i>Oryza sativa</i>	low molecular mass heat shock protein Oshsp17.7. OSHSP17.7. class I LMMHSP.
CAA63571.1	X92984	<i>Pseudotsuga menziesii</i>	low molecular weight heat-shock protein.
SEQ ID NO: 901			
AAG08959.1	AF122051	<i>Solanum tuberosum</i>	tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAG08960.1	AF122052	<i>Solanum tuberosum</i>	tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAG08961.1	AF122053	<i>Solanum tuberosum</i>	tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAF67053.1	AF190304	<i>Adiantum raddianum</i>	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF67052.1	AF190303	<i>Adiantum raddianum</i>	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF34434.1	AF172282	<i>Oryza sativa</i>	myb-like protein. DUPR11.29.

AAF78888.1	AF189786	Physcomitrella patens	putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.
AAF78887.1	AF189785	Physcomitrella patens	putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.
AAF43043.1	AF236059	Papaver rhoeas	putative Myb-related domain. pmr.
BAA94769.1	AP001859	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4, BAC clone F4D11; putative myb-protein. (AL022537).
AAF78890.1	AF189788	Hordeum vulgare	putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.
AAF78889.1	AF189787	Hordeum vulgare	putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.
BAA88169.1	AP000836	Oryza sativa	Similar to putative transcription factor (AF062890).
BAA88205.1	AP000837	Oryza sativa	Similar to putative transcription factor (AF062890).
CAA78388.1	Z13998	Petunia x hybrida	DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb proto-oncoproteins.
AAF67051.1	AF190302	Secale cereale	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF67050.1	AF190301	Secale cereale	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAG28525.1	AF198498	Nicotiana tabacum	anther-specific myb-related protein 2. mybAS2. NtMYBAS2; contains tandem R2, R3 myb domains similar to c-myb family.
BAB12688.1	AP002746	Oryza sativa	putative MYB family transcription factor. P0671B11.3. contains ESTs AU082307(E0784),C72014(E0784).
BAA99440.1	AP002743	Oryza sativa	putative MYB family transcription factor. P0710E05.27. contains ESTs AU082307(E0784),C72014(E0784).
AAK19619.1	AF336286	Gossypium hirsutum	GHMYB9. ghmyb9. similar to myb.
CAA64615.1	X95297	Lycopersicon esculentum	transcription factor. THM1. myb-related.
BAA81730.1	AB029159	Glycine max	GmMYB29A1.
CAA50224.1	X70879	Hordeum vulgare	MybHv1. myb1.
CAA50222.1	X70877	Hordeum vulgare	MybHv1. myb1.

CAB40189.1	AJ133638	Avena sativa	transcriptional activator. myb protein. gamyb.
AAG28526.1	AF198499	Nicotiana tabacum	anther-specific myb-related protein 1. myBAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.
AAD31395.1	AF114162	Lolium temulentum	gibberellin MYB transcription factor. GAMyb. R2/R3-MYB.
BAA81732.1	AB029161	Glycine max	GmMYB29A2.
BAA81731.1	AB029160	Glycine max	GmMYB29A1.
CAA61021.1	X87690	Hordeum vulgare	transcriptional activator of alpha-amylase gene promoter. GAMyb protein. Gam1.
AAG22863.1	AY008692	Hordeum vulgare	transcription factor GAMyb. Gamyb.
BAA96421.1	AB044084	Triticum aestivum	transcription activator for gibberellin response. GAMyb protein. Ta-GAMyb.
BAA81733.2	AB029162	Glycine max	GmMYB29A2.
BAA81736.1	AB029165	Glycine max	GmMYB29B2.
AAA33067.1	L04497	Gossypium hirsutum	MYB A; putative.
BAB39972.1	AP003018	Oryza sativa	putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).
CAA72218.1	Y11415	Oryza sativa	myb.
CAA67000.1	X98355	Oryza sativa	activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.
BAB39987.1	AP003020	Oryza sativa	putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
CAA78387.1	Z13997	Petunia x hybrida	DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
CAA72217.1	Y11414	Oryza sativa	myb.
BAA23341.1	D88621	Oryza sativa	transfactor. OSMYB5. Osmyb5.

BAA93038.1	AP001552	Oryza sativa	EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).
CAA64614.1	X95296	Lycopersicon esculentum	transcription factor. THM27. myb-related.
AAK19616.1	AF336283	Gossypium hirsutum	GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.
CAA78386.1	Z13996	Petunia x hybrida	DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
CAA67575.1	X99134	Lycopersicon esculentum	transcription factor. THM6. myb-related.
BAA88222.1	AB028650	Nicotiana tabacum	myb-related transcription factor LBM2. lbm2.
SEQ ID NO: 902			
CAA57773.1	X82329	Arachis hypogaea	chitinase (class II). chi2;1.
AAD54935.1	AF141373	Petroselinum crispum	random hydrolysis of 1,4-beta-acetamido-2-deoxy-D-glucoside linkages in chitin. chitinase precursor. Chi2-1. class II.
AAD54936.1	AF141374	Petroselinum crispum	random hydrolysis of 1,4-beta-acetamido-2-deoxy-D-glucoside linkages in chitin. chitinase precursor. Chi2-2. class II.
AAF00131.1	AF147091	Fragaria x ananassa	chitin degradation. class II chitinase. Chi2-1.
AAC95376.1	AF105426	Cynodon dactylon	chitinase. Cht2.
BAA95846.1	AP002070	Oryza sativa	Similar to Oryza sativa clone RGCH7 chitinase. (AF013581).
AAA32986.1	M95835	Brassica napus	endochitinase. Ch25.
AAF69783.1	AF135143	Arabis lemmonii	class I chitinase.
AAF69775.1	AF135135	Arabis drummondii	class I chitinase.
AAF69792.1	AF135152	Arabis parishii	class I chitinase.
AAC95375.1	AF105425	Cynodon dactylon	chitinase. Cht1.
AAF69785.1	AF135145	Arabis lignifera	class I chitinase.



AAF69770.1	AF135130	<i>Arabis holboellii</i> class I chitinase.
AAF69781.1	AF135141	<i>Arabis gunnisoniana</i> class I chitinase.
AAF69777.1	AF135137	<i>Arabis fecunda</i> class I chitinase.
AAF69790.1	AF135150	<i>Arabis microphylla</i> class I chitinase.
AAF69787.1	AF135147	<i>Arabis lignifera</i> class I chitinase.
AAF69772.1	AF135132	<i>Arabis gunnisoniana</i> class I chitinase.
AAF69782.1	AF135142	<i>Halimolobos perplexa</i> var. <i>perplexa</i> class I chitinase.
AAF69784.1	AF135144	<i>Arabis lemmonii</i> class I chitinase.
AAF69788.1	AF135148	<i>Arabis lyallii</i> class I chitinase.
BAA03750.1	D16222	<i>Oryza sativa</i> endochitinase. Cht-2.
AAF69776.1	AF135136	<i>Arabis fecunda</i> class I chitinase.
CAA40107.1	X56787	<i>Oryza sativa</i> chitinase.
BAB13369.1	AB048531	<i>Psophocarpus tetragonolobus</i> class I chitinase.
AAF69778.1	AF135138	<i>Arabis glabra</i> class I chitinase.
AAF69786.1	AF135146	<i>Arabis lignifera</i> class I chitinase.
BAA82826.1	AB023464	<i>Arabis gemmifera</i> basic endochitinase. ChiB.
AAF69773.1	AF135133	<i>Arabis blepharophylla</i> class I chitinase.
AAF69791.1	AF135151	<i>Arabis microphylla</i> class I chitinase.
AAF69793.1	AF135153	<i>Arabis parishii</i> class I chitinase.
CAA39535.1	X56063	<i>Oryza sativa</i> chitinase.
BAA03749.1	D16221	<i>Oryza sativa</i> endochitinase. Cht-1.

AAF69789.1	AF135149	Arabis microphylla class I chitinase.
CAA71402.1	Y10373	Medicago truncatula chitinase.
AAC16010.1	AF061805	Elaeagnus umbellata acidic chitinase.
CAA53626.1	X76041	Triticum aestivum endochitinase. CHI.
BAA33971.1	AB008892	Nicotiana tabacum chitinase 134. Chn134.
CAA47921.1	X67693	Solanum tuberosum chitinase. SK2. endochitinase.
AAF69780.1	AF135140	Arabis glabra class I chitinase.
BAB18519.1	AB051578	Secale cereale seed chitinase-a. rsca.
AAA51377.1	L37289	Oryza sativa chitinolytic activity, antifungal activity. chitinase.
AAB41324.1	U83591	Medicago sativa class I chitinase.
CAC17793.1	AJ301671	Nicotiana sylvestris hydrolysis of chitin. endochitinase. chnb. class I chitinase.
AAB41325.1	U83592	Medicago sativa class I chitinase.
AAB23263.1	S43926	Phaseolus vulgaris chitinase. CH5B. This sequence comes from Fig. 1.
AAA33756.1	M13968	Phaseolus vulgaris chitinase (EC 3.2.1.14).
CAA35945.1	X51599	Nicotiana tabacum chitinase. CHN50.
AAA34070.1	M15173	Nicotiana tabacum endochitinase precursor (EC 3.2.1.14).
CAA45822.1	X64519	Nicotiana tabacum chitinase B class I. CHN200.
SEQ ID NO: 903		
BAA78764.1	AB023482	Oryza sativa ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
AAF43496.1	AF131222	Lophopyrum elongatum protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	Lophopyrum elongatum protein kinase. ESI47.

AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461), C22360(C11461).
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808), AU056702(S20808).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAB19337.1	AP003044	Oryza sativa	putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481), AU056336(S20481).
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
AAB47424.1	U59317	Lycopersicon pimpinellifolium	serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.

AAC48932.1	U13923	<i>Lycopersicon pimpinellifolium</i> Fen. putative serine/threonine protein kinase; similar to product encoded by <i>Lycopersicon pimpinellifolium</i> Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.
AAF76307.1	AF220602	<i>Lycopersicon pimpinellifolium</i> Fen kinase.
BAA92221.1	AP001278	<i>Oryza sativa</i> Similar to <i>Arabidopsis thaliana</i> chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	<i>Oryza sativa</i> Similar to putative Ser/Thr protein kinase. (AC004218).
AAB61708.1	U93048	<i>Daucus carota</i> somatic embryogenesis receptor-like kinase. SERK.
AAK11566.1	AF318490	<i>Lycopersicon hirsutum</i> Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
AAK11568.1	AF318492	<i>Lycopersicon hirsutum</i> Pto-like protein kinase B. LhirPtoB.
AAD21872.1	AF078082	<i>Phaseolus vulgaris</i> receptor-like protein kinase homolog RK20-1.
AAF66615.1	AF142596	<i>Nicotiana tabacum</i> LRR receptor-like protein kinase.
AAC23542.1	U20948	<i>Ipomoea trifida</i> receptor protein kinase. IRK1.
AAF91337.1	AF249318	<i>Glycine max</i> PtiI kinase-like protein. PtiIb. protein kinase.
AAC27894.1	AF023164	<i>Zea mays</i> leucine-rich repeat transmembrane protein kinase 1. ltk1.
AAF76314.1	AF220603	<i>Lycopersicon esculentum</i> Fen kinase. Lescfen.
AAB47422.1	U59318	<i>Lycopersicon esculentum</i> serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.
AAF76313.1	AF220603	<i>Lycopersicon esculentum</i> Pto kinase. LescPth5.
AAB47421.1	U59316	<i>Lycopersicon esculentum</i> serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
AAF91336.1	AF249317	<i>Glycine max</i> PtiI kinase-like protein. PtiIa. protein kinase.
AAK11567.1	AF318491	<i>Lycopersicon hirsutum</i> Pto-like protein kinase F. LhirPtoF.
AAC61805.1	U28007	<i>Lycopersicon esculentum</i> serine/threonine protein kinase. Pto kinase interactor 1. Pti1. Pti1 kinase.

AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
AAF76306.1	AF220602	Lycopersicon pimpinellifolium	Pto kinase.
AAB47423.1	U59315	Lycopersicon pimpinellifolium	serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
BAB21241.1	AP002953	Oryza sativa	Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721),D48017(S13927).
AAC48914.1	U02271	Lycopersicon pimpinellifolium	protein kinase.
SEQ ID NO: 904			
AAF65545.1	AF233894	Perilla citriodora	limonene synthase.
AAG31437.1	AF241792	Perilla frutescens	limonene synthase.
AAK06663.1	AF317695	Perilla frutescens var. frutescens	limonene synthase.
AAG31435.1	AF241790	Perilla citriodora	limonene synthase.
BAA21629.1	AB005744	Perilla frutescens	catalyzing the cyclization of geranyl pyrophosphate to 1-limonene. 1-limonene synthase. gPFLC. similar to perilla PFLC-1:DDBJ Acc#D49368.
AAG31438.1	AF241793	Perilla frutescens	limonene synthase.
BAA08367.1	D49368	Perilla frutescens	limonene cyclase.
AAC37366.1	L13459	Mentha spicata	4S-limonene synthase.
AAD50304.1	AF175323	Mentha longifolia	limonene synthase. monoterpene synthase.
AAG01140.1	AF282875	Schizonepeta tenuifolia	(+)-4R-limonene synthase.
AAF21053.1	AF212433	Capsicum annuum	UV-induced sesquiterpene cyclase. SC2.

BAA82141.1	AB023816	Solanum tuberosum	vetispiradiene synthase. PVS4. potato sesquiterpene cyclase.
AAF74977.1	AF270425	Gossypium hirsutum	(E,E)-farnesyl diphosphate cyclase. (+)-delta-cadinene synthase. cdn2. sesquiterpene cyclase.
BAA82092.1	AB022598	Solanum tuberosum	vetispiradiene synthase. PVS1. potato sesquiterpene cyclase.
BAA82109.1	AB022720	Solanum tuberosum	vetispiradiene synthase. PVS3. potato sesquiterpene cyclase; PVS3.
AAG09949.1	AF171216	Lycopersicon esculentum	vetispiradiene synthase. LEVS2. sesquiterpene cyclase.
BAA82108.1	AB022719	Solanum tuberosum	vetispiradiene synthase. PVS2. potato sesquiterpene cyclase; PVS2.
AAC12784.1	U88318	Gossypium hirsutum	(E,E)-farnesyl diphosphate cyclizing. (+)-delta-cadinene synthase. cdn1. sesquiterpene cyclase; delta-cadinene synthase.
AAK15641.1	AF326117	Capsicum annum	sesquiterpene cyclase. PSC2.
AAC61260.1	AF061285	Capsicum annum	sesquiterpene cyclase. UV induced.
AAG24640.2	AF304444	Artemisia annua	sesquiterpene cyclase.
CAC12731.1	AJ271792	Artemisia annua	putative sesquiterpene cyclase. cASC125.
SEQ ID NO: 905			
AAF64450.1	AF239928	Euphorbia esula	glutathione S-transferase. similar to auxin-inducible GST.
AAG34803.1	AF243368	Glycine max	glutathione S-transferase GST 13.
AAG16759.1	AY007561	Lycopersicon esculentum	putative glutathione S-transferase T4.
AAG34798.1	AF243363	Glycine max	glutathione S-transferase GST 8.
AAG34797.1	AF243362	Glycine max	glutathione S-transferase GST 7.
AAG16758.1	AY007560	Lycopersicon esculentum	putative glutathione S-transferase T3.
AAG34809.1	AF243374	Glycine max	glutathione S-transferase GST 19.
AAG34801.1	AF243366	Glycine max	glutathione S-transferase GST 11.
AAG34796.1	AF243361	Glycine max	glutathione S-transferase GST 6.

AAG34807.1	AF243372	Glycine max glutathione S-transferase GST 17.
AAG16757.1	AY007559	Lycopersicon esculentum putative glutathione S-transferase T2.
AAG16756.1	AY007558	Lycopersicon esculentum putative glutathione S-transferase T1.
AAG34804.1	AF243369	Glycine max glutathione S-transferase GST 14.
AAG34810.1	AF243375	Glycine max glutathione S-transferase GST 20.
AAG34808.1	AF243373	Glycine max glutathione S-transferase GST 18.
AAG34805.1	AF243370	Glycine max glutathione S-transferase GST 15.
AAG34844.1	AF244701	Zea mays glutathione S-transferase GST 36.
AAG34829.1	AF244686	Zea mays glutathione S-transferase GST 21.
AAG34831.1	AF244688	Zea mays glutathione S-transferase GST 23.
AAA68430.1	J03679	Solanum tuberosum glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.
AAC18566.1	AF048978	Glycine max 2,4-D inducible glutathione S-transferase. GSTa.
AAG34832.1	AF244689	Zea mays glutathione S-transferase GST 24.
AAG34800.1	AF243365	Glycine max glutathione S-transferase GST 10.
AAG34849.1	AF244706	Zea mays glutathione S-transferase GST 41.
AAG34837.1	AF244694	Zea mays glutathione S-transferase GST 29.
AAC32118.1	AF051214	Picea mariana probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAG41204.1	AF321437	Suaeda maritima glutathione transferase.
AAG34802.1	AF243367	Glycine max glutathione S-transferase GST 12.
AAF29773.1	AF159229	Gossypium hirsutum glutathione S-transferase. GST.
AAG32472.1	AF309379	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU3.

AAG34836.1	AF244693	Zea mays	glutathione S-transferase GST 28.
CAA04391.1	AJ000923	Carica papaya	glutathione transferase. PGST1.
CAA71784.1	Y10820	Glycine max	glutathione transferase.
CAA09187.1	AJ010448	Alopecurus myosuroides	glutathione transferase. GST1a.
AAG34795.1	AF243360	Glycine max	glutathione S-transferase GST 5.
CAA09188.1	AJ010449	Alopecurus myosuroides	glutathione transferase. GST1b.
AAG34806.1	AF243371	Glycine max	glutathione S-transferase GST 16.
CAC24549.1	AJ296343	Cichorium intybus x Cichorium endivia	glutathione S-transferase. chi-GST1, auxin-induced GST.
AAC28101.1	AF079511	Mesembryanthemum crystallinum	glutathione S-transferase.
SEQ ID NO: 907			
AAA33280.1	L20475	Datura stramonium	29kDa protein; high homology to aa sequence of tropinone reductases.
AAA33281.1	L20473	Datura stramonium	catalyses a stereospecific reduction of tropinone to tropine. tropinone reductase-I.
CAC34420.1	AJ307584	Solanum tuberosum	tropine forming tropinone reductase. tropinone reductase I. TRI.
BAA85844.1	AB026544	Hyoscyamus niger	tropinone reductase-I. tr1.
BAA13547.1	D88156	Hyoscyamus niger	tropinone reductase-I.
AAA33282.1	L20474	Datura stramonium	catalyses a stereospecific reduction of tropinone to pseudotropine. tropinone reductase-II.
AAB09776.1	L20485	Hyoscyamus niger	tropinone reductase-II.
BAA85845.1	AB026545	Hyoscyamus niger	tropinone reductase-II. tr2.
CAB52307.1	AJ245634	Solanum tuberosum	pseudotropine forming tropinone reductase. tropinone reductase II. TRII.
CAC19810.1	AJ292343	Solanum tuberosum	pseudotropine forming tropinone reductase. tropinone reductase II. trII.
CAA45866.1	X64566	Cuphea lanceolata	beta-ketoacyl-ACP reductase. Clkr27. 3-oxoacyl-[acyl-carrier protein] reductase.



CAA45793.1	X64463	Brassica napus	3-oxoacyl-[acyl-carrier protein] reductase.
AAB82767.1	U89509	Zea mays	cuticular wax biosynthesis. b-keto acyl reductase. glossy8.
AAB82766.1	U89510	Hordeum vulgare	cuticular wax biosynthesis. b-keto acyl reductase. glossy8.
CAA74176.1	Y13861	Nicotiana tabacum	enoyl-ACP reductase. enr-T2.
AAB20114.2	S60064	Brassica napus	enoyl-acyl carrier protein reductase. This sequence comes from fig3; conceptual translation differs from published sequence.
CAA74177.1	Y13862	Nicotiana tabacum	enoyl-ACP reductase. enr-T1.
AAC78100.1	AF093628	Oryza sativa	protochlorophyllide reductase homolog.
CAA05879.1	AJ003124	Petunia x hybrida	enoyl-ACP reductase. pte.
CAA64729.1	X95462	Brassica napus	enoyl reductase.
CAA05816.1	AJ003025	Oryza sativa	enoyl-ACP reductase.
BAA99570.1	AB036823	Chlorella vulgaris	oxidoreductase. oxi.
SEQ ID NO: 909			
BAA82107.1	AB022693	Nicotiana tabacum	transcription factor. NtWRKY1.
AAC31956.1	AF080595	Pimpinella brachycarpa	zinc finger protein. ZFP1. WRKY1.
AAD55974.1	AF121353	Petroselinum crispum	zinc-finger type transcription factor WRKY1. WRKY1.
BAA77383.1	AB020590	Nicotiana tabacum	transcription factor NtWRKY2.
AAC49527.1	U48831	Petroselinum crispum	WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.
AAD32677.1	AF140554	Avena sativa	DNA-binding protein WRKY1. wrky1. putative transcription factor.
CAA88326.1	Z48429	Avena fatua	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAD16139.1	AF096299	Nicotiana tabacum	DNA-binding protein 2. WRKY2. transcription factor.
BAA86031.1	AB026890	Nicotiana tabacum	transcription factor NtWRKY4.

AAC37515.1	L44134	Cucumis sativus	SPF1-like DNA-binding protein.
AAK16171.1	AC079887	Oryza sativa	putative DNA-binding protein. OSJNBa0040E01.10.
AAF23898.1	AF193802	Oryza sativa	zinc finger transcription factor WRKY1.
AAD16138.1	AF096298	Nicotiana tabacum	DNA-binding protein 1. WRKY1. transcription factor.
AAC49529.1	U58540	Petroselinum crispum	WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
CAB97004.1	AJ278507	Solanum tuberosum	putative transcription factor. WRKY DNA binding protein. WRKY1.
BAB19075.1	AP002744	Oryza sativa	putative DNA-binding protein homolog. P0006C01.17.
BAB19096.1	AP002839	Oryza sativa	putative DNA-binding protein homolog. P0688A04.2.
AAK16170.1	AC079887	Oryza sativa	putative DNA binding protein. OSJNBa0040E01.4.
BAB40073.1	AP003074	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
AAD38283.1	AC007789	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAB18313.1	AP002865	Oryza sativa	putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
CAA88331.1	Z48431	Avena fatua	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAC49528.1	U56834	Petroselinum crispum	DNA-binding. WRKY3. WRKY-type DNA-binding protein.
AAG35658.1	AF204925	Petroselinum crispum	transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.
BAB16432.1	AB041520	Nicotiana tabacum	WRKY transcription factor Nt-SubD48. Nt-SubD48.
AAD32676.1	AF140553	Avena sativa	DNA-binding protein WRKY3. wrky3. putative transcription factor.
AAG46150.1	AC018727	Oryza sativa	putative DNA-binding protein. OSJNBa0056G17.18.
BAA77358.1	AB020023	Nicotiana tabacum	WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.
AAG35659.1	AF204926	Petroselinum crispum	transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.
AAD27591.1	AF121354	Petroselinum crispum	binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.

CAB66338.1	AJ279697	Betula pendula wrky-type DNA binding protein. wrky.
AAF61864.1	AF193771	Nicotiana tabacum DNA-binding protein 4. WRKY4. transcription factor.
BAA87069.1	AB035271	Matricaria chamomilla elicitor-induced DNA-binding protein homolog. McWRKY1.
AAF61863.1	AF193770	Nicotiana tabacum DNA-binding protein 3. WRKY3. transcription factor.
SEQ ID NO: 910		
AAC09420.1	M68929	Mitochondrion Marchantia polymorpha rps14.
CAA33994.1	X15901	Plastid Oryza sativa ribosomal protein S14. rps14.
SEQ ID NO: 911		
CAA55128.1	X78325	Nicotiana tabacum chitinase/lysozyme. Pz.
CAA54373.1	X77110	Nicotiana tabacum chitinase, class V. chi-V.
CAA54374.1	X77111	Nicotiana tabacum chitinase, class V. chi-V.
SEQ ID NO: 912		
CAB55394.1	AL117264	Oryza sativa zwh0010.1. similar to Arabidopsis germin-like protein 6 (AF032976); Method: conceptual translation with partial peptide sequencing.
BAA78563.1	AB024338	Atriplex lentiformis germin-like protein.
AAB97470.1	AF042489	Oryza sativa germin-like protein 16. glp16.
AAA33030.1	M93041	Mesembryanthemum crystallinum germin-like protein. germin-like protein.
CAB65371.1	AJ250834	Pisum sativum germin-like protein. ger2b. 2nd variant of the clone PsGER2.
CAB55559.1	AJ237943	Triticum aestivum germin-like protein. glp2b.
CAB65370.1	AJ250833	Pisum sativum germin-like protein. ger2a. 1st variant of this clone.
CAB55558.1	AJ237942	Triticum aestivum germin-like protein. glp2a.
AAD43971.1	AF141878	Oryza sativa germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.

AAD43973.1	AF141880	Oryza sativa	germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.
AAC04837.1	AF032976	Oryza sativa	germin-like protein 6. GER6. similar to wheat and barley oxalate oxidase.
AAG00425.1	AF250933	Hordeum vulgare	germin A. GerA. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAD43972.1	AF141879	Oryza sativa	germin-like protein 2 precursor. RGLP2. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.
CAA63659.1	X93171	Hordeum vulgare	oxalate oxidase-like protein or germin-like protein.
AAC04833.1	AF032972	Oryza sativa	germin-like protein 2. GER2. similar to wheat and barley oxalate oxidase.
AAC04834.1	AF032973	Oryza sativa	germin-like protein 3. GER3. similar to wheat and barley oxalate oxidase.
AAC04832.1	AF032971	Oryza sativa	germin-like protein 1. GER1. similar to wheat and barley oxalate oxidase.
AAG00426.1	AF250934	Hordeum vulgare	germin B. GerB. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAG00427.1	AF250935	Hordeum vulgare	germin F. GerF. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAF34811.1	AF005084	Triticum aestivum	oxalate oxidase. up-regulated by aluminum.
AAC04835.1	AF032974	Oryza sativa	germin-like protein 4. GER4. similar to wheat and barley oxalate oxidase.
BAB39965.1	AP003018	Oryza sativa	probable germin protein 4. OSJNBa0004B13.19. contains ESTs AU101991(S4037),AU070167(R0031).
BAB39980.1	AP003020	Oryza sativa	probable germin protein 4. P0498A12.8. contains ESTs AU101991(S4037),AU070167(R0031).
AAG00428.1	AF250936	Hordeum vulgare	germin D. GerD. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAA20245.1	U01963	Hordeum vulgare	germin subunit.
CAC19429.1	AJ291825	Lolium perenne	oxalate oxidase. oxO1.
AAA34270.1	M63223	Triticum aestivum	germin. germin 9f-2.8.
AAA34268.1	M21962	Triticum aestivum	germin protein precursor.

CAA74595.1	Y14203	Hordeum vulgare	oxalate oxidase.
AAG00429.1	AF250937	Hordeum vulgare	germin E. GerE. apoplastic protein.
CAB65369.1	AJ250832	Pisum sativum	germin-like protein. ger1.
AAA32959.1	L15737	Hordeum vulgare	oxalate oxidase. This is the sequence of the complete mature peptide.
CAA71052.1	Y09917	Triticum aestivum	germin homolog. pSBGer3.
AAA34271.1	M63224	Triticum aestivum	germin. germin 9f-3.8.
CAA71050.1	Y09915	Triticum aestivum	germin homolog. pSBGer1.
BAB18339.1	AP002865	Oryza sativa	putative germin protein. P0034C11.30. contains EST C97263(C53484).
AAD38298.1	AC007789	Oryza sativa	putative oxalate oxidase (germin protein). OSJNBa0049B20.25.
BAA86880.1	AB028454	Barbula unguiculata	germin-like protein.
AAF03355.1	AF132671	Nicotiana plumbaginifolia	nectarin I precursor. NEC1. germin-like protein.
BAA25197.1	AB012138	Lycopersicon esculentum	adaptation to Mn-deficiency. germin-like protein. Mdip1.
AAC78470.1	AF067731	Solanum tuberosum	germin-like protein. OXAOXA. similar to oxalate oxidase.
AAC25777.1	AF072694	Oryza sativa	germin-like protein 7. GER7. similar to wheat and barley oxalate oxidase.
AAC99473.1	AF039201	Pinus caribaea	germin-like protein. PcGER1.
CAA71051.1	Y09916	Triticum aestivum	germin homolog. pSBGer2.
AAC05146.1	AF049065	Pinus radiata	germin-like protein. PRGer1.
CAC34417.1	AJ311624	Pisum sativum	Germin-like protein. glp3.
SEQ ID NO: 915			
BAB19363.1	AP002542	Oryza sativa	putative beta-1,3-glucanase. P0679C08.2.
AAD10386.1	U72255	Oryza sativa	beta-1,3-glucanase precursor. Gns9.

CAB85903.1	AJ251646	Pisum sativum	hydrolysis of beta-1,3 conjugated glucans. beta-1,3 glucanase. gns2.
AAA90953.1	U30323	Triticum aestivum	beta 1,3-glucanase. Glc1.
BAA89481.1	AB029462	Salix gilgiana	beta-1,3-glucanase. SgGN1.
BAB40807.1	AB052291	Pyrus pyrifolia	catalyzing the hydrolysis of 1,3-beta-glucosyl linkages. endo-1,3-beta-glucanase-like protein. bgn-1. Amino acid alignment of the protein(BGN-1) encoded by pear pollen bgn-1 with barley endo-1,3-beta-glucanase(GII. accession number: pdb/1GHS-B/2.3/2/306/N/)(40% identity) and their hydrophobic cluster analysis(HCA)(a overall HCA homology score of 87.1%) showed that it was most likely that the bgn-1 encoded a endo-1,3-beta-glucanase. A higher identity(59.3%) was found between BGN-1 and a putative pea endo-1,3-beta-glucanase (accession number: dad/AJ251646-1).
AAB82772.2	AF001523	Musa acuminata	beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
CAA49513.1	X69887	Brassica napus	beta-1,3-glucanase homologue.
AAF08679.1	AF004838	Musa acuminata	beta-1,3-glucanase.
CAA82271.1	Z28697	Nicotiana tabacum	beta-1,3-glucanase.
AAD10384.1	U72253	Oryza sativa	beta-1,3-glucanase precursor. Gns7.
CAB71021.1	AJ271598	Hieracium piloselloides	putative role in callose degradation. putative beta-1,3-glucanase. gluc.
CAA30261.1	X07280	Nicotiana plumbaginifolia	beta-glucanase.
AAA51643.1	M23120	Nicotiana plumbaginifolia	beta-glucanase precursor.
AAA87456.1	U22147	Hevea brasiliensis	beta-1,3-glucanase. HGN1. hydrolytic enzyme.
AAA34078.1	M63634	Nicotiana plumbaginifolia	regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.
AAD10385.1	U72254	Oryza sativa	beta-1,3-glucanase precursor. Gns8.
CAB38443.1	AJ133470	Hevea brasiliensis	beta-1,3-glucanase. hgn1.
AAB03501.1	U41323	Glycine max	beta-1,3-glucanase. SGN1.
AAA32939.1	M62907	Hordeum vulgare	hydrolysis of beta-(1-3)-glucan. (1-3)-beta-glucanase. cBGL32.

AAD33881.1	AF141654	Nicotiana tabacum
beta-1,3-glucanase. GGL4.		
AAA03617.1	M80604	Lycopersicon esculentum
beta-1,3-glucanase.		
BAA77786.1	AB027431	Oryza sativa
beta-1,3-glucanase.		
BAA77787.1	AB027432	Oryza sativa
beta-1,3-glucanase.		
CAB91554.1	AJ277900	Vitis vinifera
beta 1-3 glucanase. gl.		
AAC14399.1	AF030771	Hordeum vulgare
beta-1,3-glucanase 2. BGL32.		
CAA03908.1	AJ000081	Citrus sinensis
glucan hydrolase. beta-1,3-glucanase. gns1.		
AAG24921.1	AF311749	Hevea brasiliensis
beta-1,3-glucanase.		
AAA33946.1	M37753	Glycine max
beta-1,3-endoglucanase (EC 3.2.1.39).		
AAA63542.1	M59443	Nicotiana tabacum
acidic beta-1,3-glucanase. glucanase.		
AAD28732.1	AF112965	Triticum aestivum
beta-1,3-glucanase precursor. Glb3.		
AAD10381.1	U72250	Oryza sativa
beta-1,3-glucanase precursor. Gns4.		
CAA57255.1	X81560	Nicotiana tabacum
(1-)-beta-glucanase. Sp41a.		
AAD33880.1	AF141653	Nicotiana tabacum
beta-1,3-glucanase. GGL1.		
AAB86541.1	AF030166	Oryza sativa
glucanase. glul.		
AAA63539.1	M60402	Nicotiana tabacum
glucan beta-1,3-glucanase. glucanase GLA.		
AAA34053.1	M60464	Nicotiana tabacum
beta-1,3-glucanase.		
AAD10380.1	U72249	Oryza sativa
beta-1,3-glucanase precursor. Gns3.		
AAA63540.1	M60403	Nicotiana tabacum
glucan-1,3-beta-glucosidase. glucanase GLB.		
SEQ ID NO: 916		
AAA85440.1	U32624	Sorghum bicolor
cytochrome P-450. CYP79. P450TYR; N-hydroxylase.		

AAF27289.1	AF140613	Manihot esculenta	N-hydroxylating cytochrome P450. CYP79D1.
AAF27290.1	AF140614	Manihot esculenta	N-hydroxylating cytochrome P450. CYP79D2.
AAD03415.1	AF069494	Sinapis alba	converts tyrosine to para-hydrophenylacetaldoxime in para-hydroxybenzylglucosinolate biosynthesis. cytochrome P450. CYP79B1.
AAG59648.1	AC084319	Oryza sativa	putative cytochrome p450tyr. OSJNBa0004B24.15.
AAF66543.1	AF140609	Triglochin maritimum	cytochrome P450 CYP79E1. CYP79E1.
AAF66544.1	AF140610	Triglochin maritimum	cytochrome P450 CYP79E2. CYP79E2.
BAA92894.1	AB006790	Petunia x hybrida	cytochrome P450. IMT-2.
AAB94587.1	AF022458	Glycine max	CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAC32274.1	AF081575	Petunia x hybrida	flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.
AAD56282.1	AF155332	Petunia x hybrida	flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
CAA64635.1	X95342	Nicotiana tabacum	cytochrome P450. hsr515. hypersensitivity-related gene.
CAA50155.1	X70824	Solanum melongena	flavonoid hydroxylase (P450). CYP75.
AAG44132.1	AF218296	Pisum sativum	cytochrome P450. P450 isolog.
AAA32913.1	M32885	Persea americana	cytochrome P-450LXXIA1 (cyp71A1).
BAA84071.1	AB028151	Antirrhinum majus	flavone synthase II. cytochrome P450. AFNS2.
AAD38930.1	AF135485	Glycine max	cytochrome P450 monooxygenaseCYP93D1. CYP93E1.
AAB17562.1	U72654	Eustoma grandiflorum	flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
AAG34695.1	AF313492	Matthiola incana	putative cytochrome P450.
CAA65580.1	X96784	Nicotiana tabacum	cytochrome P450. hsr515.
BAA93634.1	AB025016	Lotus japonicus	cytochrome P450.
CAA71513.1	Y10489	Glycine max	putative cytochrome P450.



AAB94590.1	AF022461	Glycine max	CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
CAA71876.1	Y10982	Glycine max	putative cytochrome P450.
BAA12159.1	D83968	Glycine max	Cytochrome P-450 (CYP93A1).
AAG14962.1	AF214008	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H2.
BAA74465.1	AB022732	Glycyrrhiza echinata	cytochrome P450. CYP Ge-31.
BAA22422.1	AB001379	Glycyrrhiza echinata	cytochrome P450. CYP81E1.
AAG14961.1	AF214007	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H1.
CAA04117.1	AJ000478	Helianthus tuberosus	fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'-race).
CAA04116.1	AJ000477	Helianthus tuberosus	fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
AAB94593.1	AF022464	Glycine max	CYP77A3p. CYP77A3. cytochrome P450 monooxygenase.
BAA13076.1	D86351	Glycine max	cytochrome P-450 (CYP93A2).
CAA50647.1	X71656	Solanum melongena	P450 hydroxylase.
SEQ ID NO: 918			
CAA06223.1	AJ004923	Lycopersicon esculentum	Squalene epoxidase. ERG.
SEQ ID NO: 919			
AAF71823.1	AF153276	Populus tremula x Populus tremuloides	pumilio domain-containing protein PPD1. PPD1. similar to Drosophila pumilio protein RNA-binding domain.
SEQ ID NO: 920			
BAA82393.1	AP000367	Oryza sativa	EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).
CAC20842.1	AJ250467	Pinus sylvestris	receptor protein kinase. upk.
AAB36558.1	U77888	Ipomoea nil	receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.
AAF91324.1	AF244890	Glycine max	receptor-like protein kinase 3. RLK3. GmRLK3.

BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.
AAC36318.1	AF053127	Malus x domestica	leucine-rich receptor-like protein kinase. LRPKml.
BAA84787.1	AP000559	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
BAA83373.1	AP000391	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
AAF59905.1	AF197946	Glycine max	receptor protein kinase-like protein. CLV1A.
AAK27806.1	AC022457	Oryza sativa	putative protein kinase. OSJNBa0006L06.21.
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
AAF34426.1	AF172282	Oryza sativa	leucine rich repeat containing protein kinase. DUPR11.16.
AAK27817.1	AC022457	Oryza sativa	putative protein kinase. OSJNBa0006L06.16.
CAA61510.1	X89226	Oryza sativa	leucine-rich repeat/receptor protein kinase. lrk2.
BAB03621.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.21.
AAB82755.1	U72725	Oryza longistaminata	receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.
BAB03629.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.30.
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
AAB82756.1	U72724	Oryza sativa	receptor kinase-like protein. Xa21 gene family member E.
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).

BAB18321.1	AP002865	Oryza sativa	putative receptor protein kinase. P0034C11.11.
BAB40081.1	AP003074	Oryza sativa	putative receptor protein kinase. OSJNBa0004G10.30.
AAD38286.1	AC007789	Oryza sativa	putative protein kinase. OSJNBa0049B20.13.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAC27894.1	AF023164	Zea mays	leucine-rich repeat transmembrane protein kinase 1. Itk1.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
BAA94519.1	AP001800	Oryza sativa	ESTs AU032341(R3918),AU071016(R10613) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4, BAC F9D16; putative receptor kinase (AL035394).
BAB07903.1	AP002835	Oryza sativa	putative receptor kinase. P0417G05.10. contains ESTs AU032341(R3918),AU071016(R10613).
SEQ ID NO: 921			
BAA96250.1	AB027617	Pyrus pyrifolia	UDP-glucose pyrophosphorylase.
BAA25917.1	AB013353	Pyrus pyrifolia	UDP-glucose pyrophosphorylase.
CAA62689.1	X91347	Hordeum vulgare	UDP-glucose pyrophosphorylase.
AAF62555.1	AF249880	Oryza sativa subsp. indica	UDP-glucose pyrophosphorylase. UDPGase.
SEQ ID NO: 922			
AAD03415.1	AF069494	Sinapis alba	converts tyrosine to para-hydroxybenzylglucosinolate biosynthesis. cytochrome P450. CYP79B1.

AAA85440.1	U32624	<i>Sorghum bicolor</i> cytochrome P-450. CYP79. P450TYR; N-hydroxylase.
AAF27289.1	AF140613	<i>Manihot esculenta</i> N-hydroxylating cytochrome P450. CYP79D1.
AAF27290.1	AF140614	<i>Manihot esculenta</i> N-hydroxylating cytochrome P450. CYP79D2.
AAG59648.1	AC084319	<i>Oryza sativa</i> putative cytochrome p450tyr. OSJNBa0004B24.15.
AAF66543.1	AF140609	<i>Triglochin maritimum</i> cytochrome P450 CYP79E1. CYP79E1.
AAF66544.1	AF140610	<i>Triglochin maritimum</i> cytochrome P450 CYP79E2. CYP79E2.
BAA92894.1	AB006790	<i>Petunia x hybrida</i> cytochrome P450. IMT-2.
AAD56282.1	AF155332	<i>Petunia x hybrida</i> flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
CAA50155.1	X70824	<i>Solanum melongena</i> flavonoid hydroxylase (P450). CYP75.
AAC32274.1	AF081575	<i>Petunia x hybrida</i> flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.
AAG34695.1	AF313492	<i>Matthiola incana</i> putative cytochrome P450.
AAA32913.1	M32885	<i>Persea americana</i> cytochrome P-450LXXIA1 (cyp71A1).
CAA64635.1	X95342	<i>Nicotiana tabacum</i> cytochrome P450. hsr515. hypersensitivity-related gene.
CAA65580.1	X96784	<i>Nicotiana tabacum</i> cytochrome P450. hsr515.
AAB94587.1	AF022458	<i>Glycine max</i> CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAB17562.1	U72654	<i>Eustoma grandiflorum</i> flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
AAG09208.1	AF175278	<i>Pisum sativum</i> wound-inducible P450 hydroxylase. CYP82A1.
AAD37433.1	AF150881	<i>Lycopersicon esculentum x Lycopersicon peruvianum</i> catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.
CAA04117.1	AJ000478	<i>Helianthus tuberosus</i> fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'-race).
CAA04116.1	AJ000477	<i>Helianthus tuberosus</i> fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

CAB43505.1	AJ239051	Cicer arietinum	cytochrome P450. cyp81E2.
AAC49188.2	U29333	Pisum sativum	cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
AAG14963.1	AF214009	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H3.
AAD38930.1	AF135485	Glycine max	cytochrome P450 monooxygenase CYP93D1. CYP93E1.
AAG14962.1	AF214008	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H2.
AAG44132.1	AF218296	Pisum sativum	cytochrome P450. P450 isolog.
AAB94588.1	AF022459	Glycine max	CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAG14961.1	AF214007	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H1.
AAB94590.1	AF022461	Glycine max	CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
CAA71513.1	Y10489	Glycine max	putative cytochrome P450.
BAA84071.1	AB028151	Antirrhinum majus	flavone synthase II. cytochrome P450. AFNS2.
CAA50442.1	X71130	Petunia x hybrida	P450 hydroxylase. PET 1.
SEQ ID NO: 924			
BAB20581.1	AB042268	Zea mays	response regulator 6. ZmRR6.
AAK14395.1	AF339732	Dianthus caryophyllus	response regulator protein. RR.
BAB20580.1	AB042267	Zea mays	response regulator 5. ZmRR5.
BAB20579.1	AB042261	Zea mays	response regulator 4. ZmRR4.
BAA85113.1	AB031012	Zea mays	response regulator 2. ZmRR2. cytokinin-inducible.
BAA82873.1	AB024291	Zea mays	response regulator. ZmRR2.
BAA75253.1	AB004882	Zea mays	response regulator. ZmCip1, cytokinin-inducible protein.
BAA85112.1	AB031011	Zea mays	response regulator 1. ZmRR1. cytokinin-inducible.

BAB17300.1	AB042260	Zea mays	response regulator. ZmRR3.
BAB20582.1	AB042269	Zea mays	response regulator 7. ZmRR7.
BAB41137.1	AB060130	Zea mays	response regulator 8. ZmRR8.
SEQ ID NO: 925			
AAA33280.1	L20475	Datura stramonium	29kDa protein; high homology to aa sequence of tropinone reductases.
AAA33281.1	L20473	Datura stramonium	catalyses a stereospecific reduction of tropinone to tropine. tropinone reductase-I.
BAA85844.1	AB026544	Hyoscyamus niger	tropinone reductase-I. tr1.
CAC34420.1	AJ307584	Solanum tuberosum	tropine forming tropinone reductase. tropinone reductase I. TRI.
BAA13547.1	D88156	Hyoscyamus niger	tropinone reductase-I.
AAA33282.1	L20474	Datura stramonium	catalyses a stereospecific reduction of tropinone to pseudotropine. tropinone reductase-II.
BAA85845.1	AB026545	Hyoscyamus niger	tropinone reductase-II. tr2.
AAB09776.1	L20485	Hyoscyamus niger	tropinone reductase-II.
CAB52307.1	AJ245634	Solanum tuberosum	pseudotropine forming tropinone reductase. tropinone reductase II. TRII.
CAC19810.1	AJ292343	Solanum tuberosum	pseudotropine forming tropinone reductase. tropinone reductase II. trII.
CAA45866.1	X64566	Cuphea lanceolata	beta-ketoacyl-ACP reductase. Clkr27. 3-oxoacyl-[acyl-carrier protein] reductase.
CAA45793.1	X64463	Brassica napus	3-oxoacyl-[acyl-carrier protein] reductase.
AAB82767.1	U89509	Zea mays	cuticular wax biosynthesis. b-keto acyl reductase. glossy8.
AAB82766.1	U89510	Hordeum vulgare	cuticular wax biosynthesis. b-keto acyl reductase. glossy8.
AAB20114.2	S60064	Brassica napus	enoyl-acyl carrier protein reductase. This sequence comes from fig3; conceptual translation differs from published sequence.
CAA74176.1	Y13861	Nicotiana tabacum	enoyl-ACP reductase. enr-T2.
AAB82764.1	U89511	Allium porrum	cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

AAC78100.1	AF093628	Oryza sativa	protochlorophyllide reductase homolog.
CAA74177.1	Y13862	Nicotiana tabacum	enoyl-ACP reductase. enr-T1.
SEQ ID NO: 927			
AAD43046.1	AF124045	Sorghum bicolor	GTP-binding protein-like. 110K5.8. terminal exon, defined by homology to maize ESTs.
SEQ ID NO: 928			
CAA09619.1	AJ011418	Lycopersicon esculentum	ubiquitin activating enzyme.
AAC32140.1	AF051239	Picea mariana	probable ubiquitin activating enzyme 2. Sb53. similar to Arabidopsis thaliana ubiquitin activating enzyme 2 encoded by GenBank Accession Number U40566.
AAA34308.1	M55604	Triticum aestivum	ubiquitin-activating enzyme E1. UBA1.
AAA34265.1	M90663	Triticum aestivum	ubiquitin activating enzyme. E1.
AAA34266.1	M90664	Triticum aestivum	ubiquitin activating enzyme. E1.
CAA71762.1	Y10804	Nicotiana tabacum	Ubiquitin activating enzyme E1. UBA1.
SEQ ID NO: 929			
CAA55693.1	X79086	Zea mays	initiator-binding protein. IBP2.
CAC19789.1	AJ251686	Catharanthus roseus	putative transcription factor. MYB-like DNA-binding protein. bpf-1.
CAA55691.1	X79085	Zea mays	initiator binding protein. IBP1.
AAF97508.1	AF242298	Oryza sativa	telomere binding protein-1. TBP1.
SEQ ID NO: 930			
AAK15447.1	AC037426	Oryza sativa	putative flavin-containing monooxygenase. OSJNBb0014I11.12.
AAK15439.1	AC037426	Oryza sativa	putative flavin-containing monooxygenase. OSJNBb0014I11.8.
BAA88198.1	AP000837	Oryza sativa	Similar to human dimethylaniline monooxygenase (AC002376).
BAA88195.1	AP000837	Oryza sativa	Similar to human dimethylaniline monooxygenase (AC002376).
BAB32703.1	AP002902	Oryza sativa	dimethylaniline monooxygenase-like protein. P0492F05.5. contains EST C72123(E1029).

BAB07916.2	AP002835	Oryza sativa	dimethylaniline monooxygenase-like protein. P0417G05.24. contains EST C72123(E1029).
SEQ ID NO: 931			
AAG38521.1	AF283536	Citrus x paradisi	cystatin-like protein. cystein proteinase inhibitor.
AAA97905.1	U51853	Glycine max	cysteine proteinase inhibitor.
CAA79954.1	Z21954	Vigna unguiculata	cysteine proteinase inhibitor.
AAB66355.1	U54702	Oryza sativa	thiol proteinase inhibitor; cysteine proteinase inhibitor. oryzacystatin. has potential for insect resistance in rice and for cancer therapeutics.
AAB24010.1	S49967	Oryza	oryzacystatin. oryzacystatin. cysteine protease inhibitor; This sequence comes from Fig. 1.
CAA60610.1	X87126	Zea mays	cysteine proteinase inhibitor. zmc-II.
BAA09666.1	D63342	Zea mays	cysteine proteinase inhibitor. gCC.
AAA32672.1	L16624	Ambrosia artemisiifolia	cystatin proteinase inhibitor.
BAA07327.1	D38130	Zea mays	inhibition against cysteine proteinases. cystatin II.
AAA97907.1	U51855	Glycine max	cysteine proteinase inhibitor.
BAB18766.1	AB038392	Triticum aestivum	cysteine proteinase inhibitor. WC61. cystatin.
BAB18767.1	AB038393	Triticum aestivum	cysteine proteinase inhibitor. WC92. cystatin.
CAA11899.1	AJ224331	Castanea sativa	cysteine proteinase inhibitor. cystatin.
AAB71505.1	U82220	Pyrus communis	cysteine protease inhibitor.
AAA79239.1	L48182	Brassica rapa	cysteine proteinase inhibitor. N-terminal deletion clone; putative.
CAA60634.1	X87168	Sorghum bicolor	cysteine proteinase inhibitor. CPI1.
AAA68150.1	L42819	Brassica rapa	cysteine protease inhibitor. N-terminal deletion clone; putative.
BAB18765.1	AB038391	Triticum aestivum	cysteine proteinase inhibitor. gWC2. cystatin.
BAB18768.1	AB038394	Triticum aestivum	cysteine proteinase inhibitor. WC83. cystatin.



AAC37479.1	L41355	Brassica rapa	cysteine proteinase inhibitor.
BAA28867.1	AB014760	Cucumis sativus	root-specific cystein protease inhibitor. cystein proteinase inhibitor.
AAD33907.1	AF143677	Artemisia vulgaris	cysteine proteinase inhibitor. CPI. pollen cystatin.
BAA89582.1	AP001073	Oryza sativa	ESTs AU067919(C10906),AU067918(C10906) correspond to a region of the predicted gene. Similar to cysteine proteinase inhibitor (D31700).
CAA72790.1	Y12068	Hordeum vulgare	cysteine proteinase inhibitor. CPI.
AAA96316.1	U51119	Brassica rapa	cysteine proteinase inhibitor. BCPI-2.
AAK15090.1	AF240007	Sesamum indicum	cystatin. cysteine proteinase inhibitor.
AAF23127.1	AF198389	Lycopersicon esculentum	cysteine proteinase inhibitor. cystatin. STC. expression induced by arachidonic acid and gamma linolenic acid.
BAA19610.1	D64115	Glycine max	cysteine proteinase inhibitor. cystatin.
BAA19608.1	D31700	Glycine max	cysteine proteinase inhibitor. cystatin.
CAA89697.1	Z49697	Ricinus communis	cysteine proteinase inhibitor.
AAF72202.1	AF265551	Manihot esculenta	cysteine protease inhibitor.
AAA97906.1	U51854	Glycine max	cysteine proteinase inhibitor.
CAA50437.1	X71124	Carica papaya	cysteine proteinase inhibitor (cystatin).
AAF23126.1	AF198388	Lycopersicon esculentum	cysteine proteinase inhibitor. cystatin. LTC. expression induced by arachidonic acid and gamma linolenic acid.
AAD13812.1	AF117334	Ipomoea batatas	cysteine proteinase inhibitor. cystatin.
AAF64480.1	AF241536	Ipomoea batatas	cysteine protease inhibitor. CYSPI.
AAK30004.1	AY028994	Dianthus caryophyllus	cysteine proteinase inhibitor. DC-CPIIn.
BAB18769.1	AB038395	Triticum aestivum	cysteine proteinase inhibitor. WC81. cystatin.
AAC32853.1	AF083253	Lycopersicon esculentum	cysteine protease inhibitor.

SEQ ID NO: 938		
CAA06486.1	AJ005340	Linum usitatissimum IAA amidohydrolase. homolog.
SEQ ID NO: 940		
BAB17350.1	AP002747	Oryza sativa putative nodulin. P0698G03.34. contains ESTs D39891(S1543),D41717(S4395),AU033037(S1543).
BAA85440.1	AP000616	Oryza sativa ESTs AU055729(S20023),AU055730(S20023) correspond to a region of the predicted gene.; similar to Medicago nodulin N21-like protein (AC004218).
CAB53493.1	AJ245900	Oryza sativa
CAA303720.1		protein. q3037.20. Similar to Medicago nodulin N21 (MtN21).
SEQ ID NO: 941		
BAA21921.1	AB006599	Petunia x hybrida ZPT2-12. C2H2 zinc finger protein, 2 finger.
BAA21922.1	AB006600	Petunia x hybrida ZPT2-13. C2H2 zinc finger protein, 2finger.
BAA19110.1	AB000451	Petunia x hybrida PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.
BAA21923.1	AB006601	Petunia x hybrida ZPT2-14. C2H2 zinc finger protein, 2 finger.
BAA21925.1	AB006603	Petunia x hybrida ZPT2-8. C2H2 zinc finger protein, 2 finger.
BAA21924.1	AB006602	Petunia x hybrida ZPT2-7. C2H2 zinc finger protein, 2finger.
BAA21920.1	AB006598	Petunia x hybrida ZPT2-11. C2H2 zinc finger protein, 2finger.
CAA60828.1	X87374	Pisum sativum putative zinc finger protein.
BAA19111.1	AB000452	Petunia x hybrida PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.
BAA21926.1	AB006604	Petunia x hybrida ZPT2-9. C2H2 zinc finger protein, 2 finger.
BAA21927.1	AB006605	Petunia x hybrida ZPT3-3. C2H2 zinc finger protein, 3 finger.
BAA96071.1	AB035133	Petunia x hybrida C2H2 zinc-finger protein ZPT3-3. ZPT3-3.
BAA21919.1	AB006597	Petunia x hybrida ZPT2-10. C2H2 zinc finger protein, 2 finger.
BAA96070.1	AB035132	Petunia x hybrida C2H2 zinc-finger protein ZPT2-10. PETHy;ZPT2-10.
CAB77055.1	Y18788	Medicago sativa putative TFIIIA (or kruppel)-like zinc finger protein.

AAB53260.1	U76554	Brassica rapa	transcription factor. zinc-finger protein-1. BR42.
AAB53261.1	U76555	Brassica rapa	zinc-finger protein BcZFP1. BcZFP1(3-2z).
BAA19114.1	AB000455	Petunia x hybrida	PETHy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.
BAA05078.1	D26085	Petunia x hybrida	zinc-finger DNA binding protein.
AAD26942.1	AF119050	Datisca glomerata	zinc-finger protein 1. zfp1. DgZFP1.
BAA05077.1	D26084	Petunia x hybrida	zinc-finger DNA binding protein.
AAB39638.1	U68763	Glycine max	putative transcription factor. SCOF-1. scof-1. zinc-finger protein.
AAC06243.1	AF053077	Nicotiana tabacum	transcription factor. osmotic stress-induced zinc-finger protein. zfp.
BAA19112.1	AB000453	Petunia x hybrida	PETHy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.
AAK01713.1	AF332876	Oryza sativa	zinc finger transcription factor ZF1.
BAA05076.1	D26083	Petunia x hybrida	zinc-finger DNA binding protein.
BAA05079.1	D26086	Petunia x hybrida	zinc-finger protein.
BAA21928.1	AB006606	Petunia x hybrida	ZPT4-4. C2H2 zinc finger protein, 4 finger.
BAA19926.1	AB000456	Petunia x hybrida	PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.
BAA19113.1	AB000454	Petunia x hybrida	PETHy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.
SEQ ID NO: 945			
AAG10793.1	AF296158	Citrus unshiu	beta-carotene hydroxylase. CHX1.
AAG33636.1	AF315289	Citrus unshiu	beta-carotene hydroxylase. CHX2. similar to beta-carotene hydroxylase of Citrus unshiu encoded by GenBank Accession Number AF296158.
AAG10430.1	AF251018	Tagetes erecta	beta hydroxylase.
CAB55625.1	Y14809	Lycopersicon esculentum	beta-carotene hydroxylase. CrtR-b1.
CAA70888.1	Y09722	Capsicum annuum	beta-carotene hydroxylase 2.

CAB55626.1	Y14810	Lycopersicon esculentum	beta-carotene hydroxylase. CrtR-b2.
CAA70427.1	Y09225	Capsicum annuum	beta-carotene hydrolase.
CAC06712.1	AJ278882	Narcissus pseudonarcissus	synthesis of zeaxanthin. beta-carotene hydroxylase.
AAD54243.1	AF162276	Haematococcus pluvialis	carotenoid hydroxylase.
SEQ ID NO: 946			
AAC18914.1	U94748	Petunia x hybrida	AN11. An11. No functional information available. Protein is involved in transcriptional regulation of anthocyanin biosynthesis in petunia. Protein contains five WD 40 repeats; WD 40 repeat protein.
SEQ ID NO: 948			
AAG52887.1	AF333386	Nicotiana tabacum	beta-expansin-like protein. PPAL. pollen allergen-like protein.
AAF72986.1	AF261273	Oryza sativa	putative cell wall loosening activity. beta-expansin. EXPB5.
AAF72990.1	AF261277	Oryza sativa	putative cell wall loosening activity. beta-expansin. EXPB9. putative group-1 pollen allergen.
BAB20817.1	AB051899	Atriplex lentiformis	beta-expansin. Al-EXP1.
AAF72984.1	AF261271	Oryza sativa	putative cell wall loosening activity. beta-expansin. EXPB3.
AAK15453.1	AC037426	Oryza sativa	beta-expansin EXPB3. OSJNBb0014I11.1.
AAF72991.1	AF261278	Oryza sativa	putative cell wall loosening activity. beta-expansin. EXPB10. putative group-1 pollen allergen.
AAK15442.1	AC037426	Oryza sativa	beta-expansin EXPB6. OSJNBb0014I11.3.
AAF72987.1	AF261274	Oryza sativa	putative cell wall loosening activity. beta-expansin. EXPB6.
AAF72983.1	AF261270	Oryza sativa	putative cell wall loosening activity. beta-expansin. EXPB1. putative group-1 pollen allergen Ory s1.
AAF72988.1	AF261275	Oryza sativa	putative cell wall loosening activity. beta-expansin. EXPB7.
AAF72989.2	AF261276	Oryza sativa	putative cell wall loosening activity. beta-expansin. EXPB8.
AAF72985.1	AF261272	Oryza sativa	putative cell wall loosening activity. beta-expansin. EXPB4.

AAK15440.1	AC037426	Oryza sativa	beta-expansin EXPB2. OSJNBb0014I11.2.
AAB61710.1	U95968	Oryza sativa	beta-expansin. EXPB2. cell wall loosening protein.
AAB37749.1	U30460	Cucumis sativus	expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
AAD38296.1	AC007789	Oryza sativa	putative expansin. OSJNBa0049B20.23.
BAB18336.1	AP002865	Oryza sativa	putative expansin. P0034C11.27.
CAC19183.1	AJ291816	Cicer arietinum	expansin.
AAG13983.1	AF297522	Prunus avium	expansin 2. Exp2. PruavExp2.
AAG01875.1	AF291659	Striga asiatica	alpha-expansin 3. Exp3.
AAG32920.1	AF184232	Lycopersicon esculentum	expansin. Exp8.
AAC96077.1	AF049350	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
AAC96078.1	AF049351	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
AAF35902.1	AF230333	Zinnia elegans	expansin 3.
BAA88200.1	AP000837	Oryza sativa	EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
AAC39512.1	AF043284	Gossypium hirsutum	expansin. GhEX1. contains N-terminal signal peptide.
AAD38297.1	AC007789	Oryza sativa	putative expansin. OSJNBa0049B20.24.
AAF32411.1	AF230278	Triphysaria versicolor	alpha-expansin 1.
BAB18338.1	AP002865	Oryza sativa	putative expansin. P0034C11.29.
AAG32921.1	AF184233	Lycopersicon esculentum	expansin. Exp10.
CAC19184.1	AJ291817	Cicer arietinum	expansin.
AAC96079.1	AF049352	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.
SEQ ID NO: 950			

CAA52213.1	X74115	<i>Picea abies</i>	short-chain alcohol dehydrogenase.
AAC35342.1	AF072449	<i>Ipomoea trifida</i>	short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
AAC35340.1	AF072447	<i>Ipomoea trifida</i>	short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
CAA11153.1	AJ223177	<i>Nicotiana tabacum</i>	short chain alcohol dehydrogenase.
CAA11154.1	AJ223178	<i>Nicotiana tabacum</i>	short chain alcohol dehydrogenase. SCANT.
AAK29646.1	AF349916	<i>Solanum tuberosum</i>	putative short-chain type alcohol dehydrogenase. GAN; similar to tomato Leert10 and maize Ts2.
AAC37345.1	L20621	<i>Zea mays</i>	alcohol dehydrogenase. short chain.
AAC35341.1	AF072448	<i>Ipomoea trifida</i>	short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
AAC35343.1	AF072450	<i>Ipomoea trifida</i>	short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
AAB57737.1	U89270	<i>Tripsacum dactyloides</i>	short-chain alcohol dehydrogenase. gynomonoeocious sex form 1. similar to <i>Zea mays</i> tasselseed 2: SwissProt Accession Number P50160.
AAF89645.1	AF169018	<i>Glycine max</i>	seed maturation protein PM34. PM34. similar to bacterial glucose and ribitol dehydrogenase.
AAF04253.1	AF097651	<i>Pisum sativum</i>	short-chain alcohol dehydrogenase SAD-C. sadC. contains the entire nucleotide binding motif of 3(alpha), 20(beta)-hydroxysteroid dehydrogenases, GXXXXXXGXXG(A)XGXXXXA (Ghosh et al., 1991, Proc. Natl. Acad. Sci. USA 88, 10064-10068).
AAF04193.1	AF053638	<i>Pisum sativum</i>	short-chain alcohol dehydrogenase. sadA. contains the entire nucleotide binding motif of the 3(alfa),20(beta)-hydroxysteroid dehydrogenase: GXXXXXXGXXG(A)XGXXXXA (Ghosh et al. (1991) Proc. Natl. Acad. Sci. USA 88, 10064-10068); similar to <i>Lycopersicon esculentum</i> product encoded by GenBank Accession Number U21801 and <i>Streptomyces hydrogenans</i> steroid alcohol dehydrogenase.
AAB57738.1	U89271	<i>Tripsacum dactyloides</i>	short-chain alcohol dehydrogenase. gynomonoeocious sex form 1. similar to <i>Zea mays</i> tasselseed 2: SwissProt Accession Number P50160.
CAB91875.1	AJ277945	<i>Lycopersicon esculentum</i>	putative alcohol dehydrogenase. yfe37.
AAF04194.1	AF053639	<i>Pisum sativum</i>	short-chain alcohol dehydrogenase. sadB. contains the Prosite pattern no. PS00061 for short-chain alcohol dehydrogenases; contains a deletion in the nucleotide binding motif of the 3(alfa),20(beta)-hydroxysteroid dehydrogenase: GXXXXXXGXXG(A)XGXXXXA (Ghosh et al. (1991) Proc. Natl. Acad. Sci. USA 88, 10064-10068).

AAB00109.1	U21801	Lycopersicon esculentum	alcohol dehydrogenase homolog. GAD3. mRNA is suppressed in the presence of gibberellin; similar to nonmetallo-short-chain alcohol dehydrogenases, PIR Accession Number A47542.
SEQ ID NO: 952			
CAB63264.1	AJ251808	Lotus japonicus	calcium-binding protein. cbp1.
AAG43547.1	AF211529	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 31. ACRE31. similar to Solanum tuberosum CAST calcium binding protein encoded by GenBank Accession Number L02830.
AAA34014.1	L01432	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAA34013.1	L01430	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-1. putative.
AAA92681.1	U13882	Pisum sativum	calcium-binding protein. calmodulin.
CAA78301.1	Z12839	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin. putative.
AAA19571.1	U10150	Brassica napus	calcium binding. calmodulin. bcm1.
AAA85157.1	U20297	Solanum tuberosum	calcium-binding protein. calmodulin.
AAA85156.1	U20296	Solanum tuberosum	calcium-binding protein. calmodulin.
AAA62351.1	U20295	Solanum tuberosum	calcium-binding protein. calmodulin.
AAA85155.1	U20294	Solanum tuberosum	calcium-binding protein. calmodulin.
AAC49587.1	U49105	Triticum aestivum	calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	Triticum aestivum	calmodulin TaCaM3-3. calcium-binding protein.
AAC49585.1	U49103	Triticum aestivum	calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum	calmodulin TaCaM3-1. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum	calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	Triticum aestivum	calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	Triticum aestivum	calmodulin TaCaM1-1. calcium-binding.

CAA78287.1	Z12827	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
AAA03580.1	L01431	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-2. putative.
AAA33901.1	L18913	Oryza sativa	calcium binding protein, signal transduction. calmodulin. putative.
AAA34015.1	L01433	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-4. putative.



**Table 24** Plant Open Reading Frames (ORFs) orthologous to specific *Chenopodium* ORFs

SEQ ID NO:1956	
CAB51903.1	AJ242807 <i>Brassica napus</i> endo-1,4-beta-D-glucanase. Cel16. cellulase.
BAA94257.1	AB040769 <i>Hordeum vulgare</i> endo-1,4-beta-glucanase Cel1. Cel1.
AAC49704.1	U78526 <i>Lycopersicon esculentum</i> endo-1,4-beta-glucanase. Cel3.
SEQ ID NO:1957	
BAB21273.1	AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.4.
BAB21275.1	AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.6.
BAB21276.1	AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
CAA94437.1	Z70524 <i>Spirodela polyrhiza</i> multidrug resistance protein. PDR5-like ABC transporter.
BAB21279.1	AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.10. contains ESTs AU065360(R3463), AU101680(R3463).
CAA03960.1	AJ000234 <i>Hordeum vulgare</i> partial sequence, homology to PDR5-like ABC transporter.
SEQ ID NO:1960	
AAD51778.1	AF116858 <i>Phaseolus vulgaris</i> utilizes UDPX as the sugar donor and catalyzes the formation of O-xylosylzeatin from zeatin. zeatin O-xylosyltransferase. ZOX1.
AAD04166.1	AF101972 <i>Phaseolus lunatus</i> catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
BAA36410.1	AB012114 <i>Vigna mungo</i> UDP-glycose:flavonoid glycosyltransferase. UFGlyT.
BAB17061.1	AP002523 <i>Oryza sativa</i> putative glucosyl transferase. P0013F10.7. contains EST C73149(E2992).

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BAA36412.1 AB012116 *Vigna mungo*  
UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

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AAK28303.1 AF346431 *Nicotiana tabacum*  
phenylpropanoid:glucosyltransferase 1. togt1.  
glucosyltransferase.

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BAB17059.1 AP002523 *Oryza sativa*  
putative glucosyl transferase. P0013F10.5.

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AAF17551.1 AF198453 *Glycine max*  
UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

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AAB36653.1 U32644 *Nicotiana tabacum*  
immediate-early salicylate-induced glucosyltransferase.  
IS5a.

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CAB88666.1 AJ400861 *Cicer arietinum*  
flavonoid glycosyltransferase. putative UDP-glycose.

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AAB36652.1 U32643 *Nicotiana tabacum*  
immediate-early salicylate-induced glucosyltransferase.  
IS10a.

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CAA54612.1 X77462 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT5.

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BAB17060.1 AP002523 *Oryza sativa*  
putative glucosyl transferase. P0013F10.6.

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AAK28304.1 AF346432 *Nicotiana tabacum*  
phenylpropanoid:glucosyltransferase 2. togt2.  
glucosyltransferase.

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CAA59450.1 X85138 *Lycopersicon esculentum*  
twil. homologous to glucosyltransferases.

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BAA83484.1 AB031274 *Scutellaria baicalensis*  
UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

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CAA54611.1 X77461 *Manihot esculenta*  
UTP-glucose glucosyltransferase. CGT2.

---

BAA36411.1 AB012115 *Vigna mungo*  
UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

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CAC35167.1 AJ310148 *Rauvolfia serpentina*  
arbutin synthase. as.

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BAB17182.1 AP002843 *Oryza sativa*  
putative UTP-glucose glucosyltransferase. P0407B12.19.

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CAB56231.1	Y18871	<i>Dorotheanthus bellidiformis</i>	betanidin-5-O-glucosyltransferase.
BAB17176.1	AP002843	<i>Oryza sativa</i>	putative UTP-glucose glucosyltransferase. P0407B12.13.
AAK16172.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.14.
CAA54613.1	X77463	<i>Manihot esculenta</i>	UTP-glucose glucosyltransferase. CGT6.
AAF61647.1	AF190634	<i>Nicotiana tabacum</i>	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAA93039.1	AB033758	<i>Citrus unshiu</i>	limonoid UDP-glucosyltransferase. LGTase.
CAA54610.1	X77460	<i>Manihot esculenta</i>	UTP-glucose glucosyltransferase. CGT4.
AAA59054.1	L34847	<i>Zea mays</i>	conjugation of the growth hormone indole-3-acetic acid (IAA). IAA-glu synthetase. iaglu.
BAA36423.1	AB013598	<i>Verbena x hybrida</i>	UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
AAF17077.1	AF199453	<i>Sorghum bicolor</i>	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.
CAA54558.1	X77369	<i>Solanum melongena</i>	glycosyl transferase. GT.
AAK16175.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.15.
CAA81057.1	Z25802	<i>Petunia x hybrida</i>	UDP rhamnose: anthocyanidin-3-glucoside rhamnosyltransferase.
CAA50377.1	X71060	<i>Petunia x hybrida</i>	anthocyanin: rhamnosyltransferase. rt.
CAA50376.1	X71059	<i>Petunia x hybrida</i>	anthocyanin 3 glucoside: rhamnosyltransferase. rt.
AAK16181.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.16.
AAK16178.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.5.

AAD21086.1	AF127218	Forsythia x intermedia
adds glucose residue to position 3 of flavonoid compounds.		
flavonoid 3-O-glucosyltransferase. UFGT.		
BAA89008.1	AB027454	Petunia x hybrida
anthocyanidin 3-O-glucosyltransferase. PGT8.		
<b>SEQ ID NO:1962</b>		
CAA65580.1	X96784	Nicotiana tabacum
cytochrome P450. hsr515.		
CAA64635.1	X95342	Nicotiana tabacum
cytochrome P450. hsr515. hypersensitivity-related gene.		
AAG44132.1	AF218296	Pisum sativum
cytochrome P450. P450 isolog.		
AAG49299.1	AF313489	Callistephus chinensis
flavonoid 3',5'-hydroxylase.		
BAA03438.1	D14588	Petunia x hybrida
flavonoid-3',5'-hydroxylase. Hfl.		
AAC32274.1	AF081575	Petunia x hybrida
flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.		
CAA50442.1	X71130	Petunia x hybrida
P450 hydroxylase. PET 1.		
CAA80266.1	Z22545	Petunia x hybrida
flavonoid 3',5'-hydroxylase.		
AAG49315.1	AF315465	Pelargonium x hortorum
flavonoid 3'-hydroxylase.		
AAG49298.1	AF313488	Callistephus chinensis
putative flavonoid 3'-hydroxylase.		
AAB17562.1	U72654	Eustoma grandiflorum
flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.		
BAB20076.1	AB012925	Torenia hybrida
flavonoid 3',5'-hydroxylase. F3'5'H.		
AAG14961.1	AF214007	Brassica napus
cytochrome p450-dependent monooxygenase. BNF5H1.		
CAC26920.1	AJ295586	Arabidopsis lyrata subsp. petraea
ferulate-5-hydroxylase. fah1.		
AAG14962.1	AF214008	Brassica napus
cytochrome p450-dependent monooxygenase. BNF5H2.		

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- 15 All publications, patents and patent applications are incorporated herein by reference.
- While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied
- 20 considerably without departing from the basic principles of the invention.

**WHAT IS CLAIMED IS:**

1. A method to identify at least one gene involved in plant resistance or response to infection by at least one pathogen comprising:
  - 5 a) determining or detecting plant gene expression in an incompatible interaction; and
  - b) identifying at least one gene whose expression is significantly altered in the incompatible interaction relative to expression of the at least one gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to infection by a pathogen, or in a corresponding compatible interaction.
- 10 2. A method to identify at least one gene involved in plant resistance or response to infection by at least one pathogen comprising:
  - a) determining or detecting plant gene expression in a compatible interaction; and
  - 15 b) identifying at least one gene whose expression is significantly altered in the compatible interaction relative to expression of the at least one gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to infection by a pathogen, or in a corresponding incompatible interaction.
- 20 3. The method of claim 1 or 2 wherein the compatible interaction is between a plant having a resistance gene and a pathogen lacking a corresponding avirulence gene, a plant lacking a resistance gene to a pathogen having a corresponding avirulence gene, or a plant lacking a resistance gene and a pathogen lacking a corresponding avirulence gene.
- 25 4. The method of claim 1 or 2 wherein expression of the at least one gene is upregulated in response to infection.
5. The method of claim 1 or 2 wherein expression of the at least one gene is downregulated in response to infection.
- 30 6. The method of claim 1 or 2 wherein the at least one gene encodes a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737.

7. The method of claim 1 or 2 wherein the at least one gene comprises an open reading frame comprising one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737.
8. The method of claim 1 or 2 wherein the pathogen is a bacterium.
9. The method of claim 1 or 2 wherein the pathogen is a fungus.
10. The method of claim 1 or 2 wherein the pathogen is a virus.
11. The method of claim 1 or 2 wherein gene expression is detected or determined using a gene chip, a cDNA array, cDNA-AFLP, or differential display PCR
12. The method of any one of claims 1 to 6 or 8 to 11 wherein the plant is a dicot.
13. The method of any one of claims 1 to 6 or 8 to 11 wherein the plant is a monocot.
14. The method of any one of claims 1 to 13 further comprising isolating the at least one gene or a portion thereof which includes the open reading frame or promoter for the gene.
15. A method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation that decreases jasmonic acid or ethylene-dependent signaling, comprising:
  - a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
  - b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having the mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant.

16. A method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation in a gene that interferes with salicylic acid dependent signaling, comprising:
- 5 a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
- 10 b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having a mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant.
- 15 17. A method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation that results in enhanced susceptibility to bacterial infection, comprising:
- 20 a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
- 25 b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having a mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant.
- 30 18. A method to identify at least one gene, the expression of which is altered by infection with at least one virus, comprising:
- a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with a virus, so as to form a

- complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
- b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from an uninfected plant, so as to identify a gene, the expression of which is altered by virus infection.
19. A method to identify at least one gene, the expression of which is altered by infection with at least one pathogen comprising:
- a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from an incompatible interaction so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
- b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from a corresponding compatible interaction so as to identify a gene, the expression of which is altered by the pathogen.
20. The method of any one of claims 15 to 19 wherein the at least one gene is upregulated.
21. The method of any one of claims 15 to 19 wherein the at least one gene is downregulated.
22. The method of any one of claims 15 to 19 wherein the gene which is identified encodes a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737.
23. The method of any one of claims 15 to 19 wherein the probes comprise nucleic acid from a dicot.
24. The method of any one of claims 15 to 19 wherein the probes comprise nucleic acid from a cereal plant.



25. The method of any one of claims 15 to 19 wherein the probes comprise nucleic acid from a monocot.
26. The method of any one of claims 15 to 19 further comprising identifying the promoter for  
5 the at least one gene.
27. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, which plant nucleotide sequence is from a gene encoding a polypeptide that is  
10 substantially similar to a polypeptide encoded by a gene comprising a promoter selected from the group consisting of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.
28. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection,  
15 which plant nucleotide sequence hybridizes under high stringency conditions to the complement of any one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.
29. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant after pathogen infection, which  
20 plant nucleotide sequence hybridizes under very high stringency conditions to the complement of any one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.
30. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, which plant  
25 nucleotide sequence is selected from the group consisting of SEQ ID NOs:2137-2661 and or SEQ ID NOs:4738-6813.
31. The polynucleotide of any one of claims 27 to 30 wherein the plant nucleotide sequence is  
30 25 to 2000 nucleotides in length.
32. The polynucleotide of any one of claims 27 to 30 wherein the plant nucleotide sequence has at least 90% nucleotide sequence identity to one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.

33. The polynucleotide of any one of claims 27 to 30 wherein the plant nucleotide sequence has at least 98% nucleotide sequence identity to one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.
- 5
34. The polynucleotide of any one of claims 27 to 29 and 31 to 33 wherein the plant nucleotide sequence is from a dicot.
35. The polynucleotide of any one of claims 26 to 29 and 31 to 33 wherein the plant  
10 nucleotide sequence is from a monocot.
36. The polynucleotide of any one of claims 26 to 29 and 31 to 33 wherein the plant nucleotide sequence is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat sequence.
- 15
37. The polynucleotide of any one of claims 27 to 36 which comprises a TATA box, a CAAT box, or both.
38. A composition comprising the polynucleotide of any one of claims 27 to 37.
- 20
39. A recombinant vector comprising the polynucleotide of any one of claims 27 to 38.
40. The vector of claim 39 which is selected from the group consisting of a plasmid, phagemid, cosmid, virus, F-factor and phage.
- 25
41. An expression cassette comprising the polynucleotide of any one of claims 27 to 37 operatively linked to an open reading frame.
42. The expression cassette of claim 41 operably linked to other suitable regulatory sequences.
- 30
43. The expression cassette of claim 41 wherein the open reading frame is in an antisense orientation relative to the nucleotide sequence which alters transcription.

44. The expression cassette of claim 41 wherein the open reading frame is in a sense orientation relative to the nucleotide sequence which alters transcription.
45. A recombinant vector comprising the expression cassette of claim 41.
- 5 46. The vector of claim 45 wherein the vector is selected from the group consisting of a plasmid, phagemid, cosmid, virus, F-factor or phage.
47. A host cell comprising the expression cassette of claim 41.
- 10 48. The host cell of claim 47 wherein the cell is selected from the group consisting of a yeast, a bacterium, a cereal plant cell, and an *Arabidopsis* cell.
49. A plant cell containing the expression cassette of claim 41.
- 15 50. The plant cell of claim 49 which is a monocot cell.
51. The plant cell of claim 49 which is a dicot cell.
- 20 52. A transformed plant, the genome of which is augmented with the expression cassette of claim 41.
53. A transformed plant comprising transformed plant cells, which cells contain the expression cassette of claim 41.
- 25 54. The transformed plant of claim 52 or 53 which is a dicot.
55. The transformed plant of claim 52 or 53 which is a monocot.
- 30 56. The transformed plant of claim 52 or 53 which is selected from the group consisting of maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat and *Arabidopsis*.

57. A method for augmenting a plant genome, comprising:
- a) contacting plant cells with the expression cassette of claim 41 so as to yield a transformed plant cell; and
  - b) regenerating the transformed plant cell to provide a differentiated transformed plant,  
5        wherein the differentiated transformed plant expresses the open reading frame in the  
      cells of the plant.
58. A method to alter the phenotype of a plant cell comprising: introducing the expression  
cassette of claim 41 into a plant cell and expressing that open reading frame in the cell so  
10        as to alter a characteristic of that cell relative to a plant cell that does not comprise the  
      expression cassette.
59. The method of claim 57 or 58 wherein the plant cell is a dicot cell.
- 15    60. The method of claim 57 or 58 wherein the plant is a monocot cell.
61. The method of claim 57 or 58 wherein the plant cell a cereal cell.
62. The method of claim 57 or 58 wherein the plant cell is selected from the group consisting  
20        of a cell of maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut,  
      sorghum, tobacco, sugarbeet, rice, wheat and *Arabidopsis*.
63. The method of claim 57 or 58 wherein the open reading frame is in an antisense  
orientation relative to the nucleotide sequence which alters transcription.  
25
64. The method of claim 57 or 58 wherein the expression inhibits transcription or translation  
of endogenous plant nucleic acid sequences corresponding to the open reading frame.
65. The method of claim 57 or 58 wherein the open reading frame is in a sense orientation  
30        relative to the nucleotide sequence which alters transcription.
66. The method of claim 57 wherein the open reading frame is expressed in an amount that is  
greater than the amount in a plant which does not comprise the expression cassette.

67. The method of claim 57 or 58 wherein the open reading frame encodes a protein.
68. The method of claim 67 wherein the protein encodes a regulatory product.
- 5 69. The method of claim 67 wherein the expression of the open reading frame confers insect resistance, bacterial resistance, fungal resistance, viral resistance, or nematode resistance.
70. A transformed plant prepared by the method of claim 57.
- 10 71. A product of the plant of claim 70 which comprises the expression cassette or the gene product encoded by the open reading frame.
72. The product of claim 71 which is selected from the group consisting of a seed, fruit,  
15 vegetable, transgenic plant, and a progeny plant.
73. A computer-readable medium having stored thereon a data structure comprising:  
a) a nucleic acid molecule that has at least 70% nucleic acid sequence identity to a  
nucleotide molecule selected from the group consisting of SEQ ID NOs:1-953, 2137-  
20 2661, 1954-1966, 2000-2129, 2662-4737, 4738-6813 or the complement thereof; and  
b) a module receiving the nucleic acid molecule which compares the nucleic acid  
sequence of the molecule to at least one other nucleic acid sequence.
74. The computer readable medium of claim 73 wherein the medium is selected from the  
25 group consisting of magnetic tape, optical disk, CD-ROM, random access memory,  
volatile memory, non-volatile memory and bubble memory.
75. A computer-readable medium having stored thereon computer executable instructions for  
performing a method comprising:  
30 a) receiving a nucleic acid molecule having at least 70% nucleic acid sequence identity to  
a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-953, 2137-  
2661, 1954-1966, 2000-2129, 2662-4737, 4738-6813 or the complement thereof; and

- b) comparing the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.
76. The computer readable medium of claim 75 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
77. The computer readable medium of any one of claims 73 to 76 wherein the nucleotide sequence is not SEQ ID NOs. 1-208, 210-215, 217-261, 263-266, 268-316, 318-385, 387-424, 426-439, 441-799, or 801-953.
78. A method to confer resistance or tolerance to a plant to a pathogen, comprising:
- a) contacting plant cells with an expression cassette comprising a polynucleotide encoding a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 so as to yield transformed cells; and
- b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the polynucleotide in the cells of the plant in an amount effective to confer resistance or tolerance to the plant to a pathogen relative to a corresponding plant which does not comprise the expression cassette.
79. The method of claim 78 wherein the polynucleotide hybridizes under moderate stringency conditions to the complement of any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737.
80. The method of any one of claims 78 to 79 wherein the cells are monocot cells.
81. The method of any one of claims 78 to 79 wherein the cells are dicot cells.
82. The method of claim 78 wherein the open reading frame encodes a DNA binding protein, hormone response protein, membrane protein, metabolic protein, transposon, receptor/kinase, phosphatase, stress protein, cell wall protein, lipid transfer protein, heat

shock protein, protein processing protein, RNA processing protein, non-cell wall structural protein or a non-kinase signaling protein.

83. A transformed plant prepared by the method of any one of claims 78 to 82.

5

84. A seed of the plant of claim 83.

85. A progeny plant of the plant of claim 83.

10 86. A method to identify a plant cell infected with a pathogen, comprising:

a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with at least one oligonucleotide under conditions effective to specifically amplify a nucleotide sequence corresponding to one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 or a portion thereof, so as to yield an amplified product; and

15

b) detecting or determining the presence or amount of the amplified product, wherein the presence or amount of the amplified product is indicative of pathogen infection.

87. A method to identify a plant cell infected with a pathogen, comprising:

20 a) contacting a sample comprising polypeptides obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds to a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 so as to form a complex, wherein the; and

25 b) detecting or determining the presence or amount of the complex, wherein the presence or amount of the complex is indicative of pathogen infection.

88. A method to identify a plant cell infected with a pathogen, comprising:

30 a) contacting nucleic acid obtained from a plant cell suspected of being infected with a pathogen with a probe corresponding to a sequence selected from the group consisting of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737 or a portion thereof, under stringent hybridization conditions to form a duplex, and

- b) detecting or determining the presence or amount of the duplex, wherein the presence of a duplex is indicative of infection.

89. A method for marker-assisted breeding to select for plants having altered

5 resistance to a pathogen comprising:

- a) contacting plant DNA or cDNA with a probe comprising a sequence selected from the group consisting of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737 or a portion thereof which hybridizes under moderate stringency conditions to a gene corresponding to one of of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737
- 10 so as to form a duplex; and

- b) detecting or determining the presence or amount of the duplex, wherein the amount or presence of the duplex is indicative of the presence of a gene, the expression of which alters the resistance of the plant to a pathogen.

15



# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/IB 01/01105

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/29 C12N15/82 C12Q1/68 A01H5/00 G06F17/00  
C07K14/415

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, MEDLINE, SEQUENCE SEARCH

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SCHENK P M ET AL: "Coordinated plant defense responses in Arabidopsis revealed by microarray analysis" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 97, no. 21, 10 October 2000 (2000-10-10), pages 11655-11660, XP002153163 ISSN: 0027-8424 the whole document	1-5, 8-21, 23-26
X	WO 97 49822 A (CIBA GEIGY AG ;ELLIS DANIEL MURRAY (US); FRIEDRICH LESLIE BETHARDS) 31 December 1997 (1997-12-31) the whole document --- -/--	1-5, 8-21, 23-26

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance  
"E" earlier document but published on or after the international filing date  
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)  
"O" document referring to an oral disclosure, use, exhibition or other means  
"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention  
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone  
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.  
"&" document member of the same patent family

Date of the actual completion of the international search

9 July 2002

Date of mailing of the international search report

25. 09. 2002

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## INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 01/01105

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01 07603 A (TUZUN SADIK ;UNIV AUBURN (US); ABDULLAH MALIKAH (US); SINGH NAREND) 1 February 2001 (2001-02-01) the whole document	1-5, 8-21, 23-26
X	EP 1 033 405 A (CERES INC) 6 September 2000 (2000-09-06)	73-76, 78-86, 88,89
A	page 1 -page 26 see SEQ IN NO: 38097 page 325 -page 341; claims 1-34 -----	6,7,22

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/IB 01/01105

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☒ Claims Nos.: 87  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:  
see FURTHER INFORMATION sheet PCT/ISA/210
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:  
Claims 1-26, 73-89 partially.
  
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 87

Present claim 87 relates to a product/compound defined by reference to a desirable characteristic or property, namely an agent that binds to a polypeptide encoded by an open reading frame.

The claims cover all products/compounds having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for only a very limited number of such products/compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the product/compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, no search has been carried out.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-26, 73-89 partially

A method to identify at least one gene involved in plant resistance or response to infection by at least one pathogen wherein the gene encodes a polypeptide encoded by an open reading frame comprising SEQ ID NO: 1. A method to identify at least one gene, the expression of which is altered by pathogen infection, a computer-readable medium, a method to confer resistance or tolerance to a plant, a transformed plant, a seed, a method to identify a plant cell infected with a pathogen, a method for marker-assisted breeding comprising said nucleic acid.

Invention 2-3173: claims 1-26, 73-89 partially

same as invention 1 but comprising a gene in the order as given in claim 6 (invention 2 is limited to SEQ ID NO: 2 and invention 3173 is limited to SEQ ID NO: 4737).

Invention 3174: claims 26-77 partially

An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid comprising SEQ ID NO: 2137. A composition, a vector, an expression cassette, a host cell, a plant cell, a transformed plant, a method for augmenting a plant genome, a method to alter the phenotype of a plant cell, a computer-readable medium comprising said polynucleotide.

Invention 3174-5774: claims 26-77 partially

same as invention 3173 but comprising a promoter sequence in the order as given in claim 27 (invention 3174 comprises SEQ ID NO: 2138 and invention 5774 comprises SEQ ID NO: 6813).

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/IB 01/01105

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